

GenCore version 5.1.6  
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protein - protein search, using sw model

on: February 18, 2004, 06:03:18 ; Search time 44 Seconds  
(without alignments)  
41.537 Million cell updates/sec

le: US-09-806-376-1

fect score: 123  
pence: 1 FNRCCCLIPACRRNKKFC 19

ring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

arched: 283366 seqs, 96191526 residues

al number of hits satisfying chosen parameters: 283366

imum DB seq length: 0

imum DB seq length: 2000000000

it-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

abase : PIR78:\*

1: PIR1:\*

2: PIR2:\*

3: PIR3:\*

4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

ult No.	Score	Query Match %	Length	DB	ID	Description
1	52	42.3	189	2	T15479	hypothetical prote
2	50.5	41.1	720	2	T25883	hypothetical prote
3	49	39.8	67	1	T1ILF2	trypsin inhibitor
4	49	39.8	67	1	T1ILF3	trypsin inhibitor
5	49	39.8	640	2	T08179	LFG5 protein - Chl
6	48	39.0	16	2	A54877	alpha-conotoxin Pn
7	48	39.0	924	2	T09220	exocyst complex pr
8	47	38.2	257	2	A45753	folate-binding pro
9	46.5	37.8	48	2	S29973	protamine 1 - guin
10	46	37.4	57	2	S42778	relaxin - gorilla
11	46	37.4	174	2	T01649	probable trypsin i
12	46	37.4	185	1	A44559	relaxin 1 precursor
13	46	37.4	363	2	A48338	hypothetical prote
14	45.5	37.0	97	2	S59427	hypothetical prote
15	45	36.6	64	1	T1OAB	trypsin inhibitor
16	45	36.6	361	2	G70862	probable adheE2 pro
17	45	36.6	410	1	QMSA1	thyroid hormone re
18	45	36.6	519	2	E4503	hypothetical prote
19	45	36.6	589	2	B38128	epithelin/granulin
20	45	36.6	593	1	G7YU	granulin precursor
21	45	36.6	749	2	S13518	transposase Tan3 -
22	44.5	36.2	50	1	HS5H	sperm histone 1 - sh
23	44.5	36.2	51	1	HS5OS	sperm histone p1 -
24	44.5	36.2	316	1	A60603	aldehyde reductase
25	44.5	36.2	316	2	T49484	aldehyde reductase
26	44.5	36.2	1743	2	T18279	multidrug resistan
27	44.5	36.2	2561	2	T24864	hypothetical prote
28	44	35.8	16	2	A59046	alpha-conotoxin MI
29	44	35.8	16	2	A59042	alpha-conotoxin Ep

ALIGNMENTS

RESULT 1

T15479

hypothetical protein C10A4.6 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 04-Mar-2000

C:Accession: T15479

R.Pauley, A.

submitted to the EMBL Data Library, March 1995

A:Description: The sequence of C. elegans cosmid C10A4.

A:Reference number: Z18358

A:Accession: T15479

A>Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-189 <PAU>

A:Cross-references: EMBL:U23454; NID:G733580; PID:G733586; PIDN:AAC46520.1; CESP:C10A4

A:Experimental source: strain Bristol N2

C:Genetics:

A:Gene: CESP:C10A4.6

A:Introns: 40/1; 91/2; 119/1; 157/2

C:Superfamily: Caenorhabditis elegans hypothetical protein C10A4.6

Query Match 42.3%; Score 52; DB 2; Length 189;

Best Local Similarity 44.4%; Pred. No. 2.7;

Matches 12; Conservative 1; Mismatches 4; Indels 10; Gaps 1;

QY 1 FNRCCCLIPA-----CRNKK 17

DB 144 FNRCCCYCATKMKLNQICRRGKK 170

RESULT 2

T25883

hypothetical protein T10E9.2 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 21-Jan-2000

C:Accession: T25883

R.Greco, T.; Hawkins, M.

submitted to the EMBL Data Library, April 1997

A:Description: The sequence of C. elegans cosmid T10E9.

A:Reference number: Z20104

A:Accession: T25883

A>Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-720 <GRE>

A:Cross-references: EMBL:U97403; PIDN:AAB52470.1; GSPDB:GN00019; CESP:T10E9.2

A:Experimental source: strain Bristol N2; clone T10E9

C:Genetics:

CAAX prenyl protei  
aldose reductase h  
hypothetical prote  
aldehyde reductase  
aldehyde reductase  
hypothetical prote  
folate-binding pro  
hypothetical prote  
folate-binding pro  
probable alcohol d  
cysteine proteinas  
hypothetical prote  
protein F52C12.4 [  
hypothetical prote  
aldehyde reductase  
laminin-related pr  
alpha-conotoxin Pn  
hypothetical prote  
SS RNA-binding pro  
hypothetical prote  
hypothetical prote

T08179  
LRGS protein - Chlamydomonas reinhardtii  
C/Species: Chlamydomonas reinhardtii  
C/Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 11-Jun-1999  
C/Accession: T08179  
R/Glossckner, G.; Beck, C.F.  
submitted to the EMBL Data Library, October 1996  
A/Description: Molecular characterization of a gene (LRG5) involved in blue light signal transduction  
A/Reference number: Z16399  
A/Accession: T08179  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: mRNA  
A/Residues: 1-640 <GLO>  
A/Cross-references: EMBL:U73817; NID:G1644369; PID:G1644370  
C/Genetics:  
A/Gene: LRG5

Query Match 39.8%; Score 49; DB 2; Length 640;  
Best Local Similarity 60.0%; Pred. No. 18;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 NWRCCLIPAC 11  
|||  
Db 586 NWVCCLPGC 595

RESULT 6  
A54877  
alpha-conotoxin Pn1A [validated] - cone shell (Conus pennaceus)  
N/Alternate names: alpha-CTX-Pn1A  
C/Species: Conus pennaceus  
C/Date: 19-Mar-1997 #sequence\_revision 25-Apr-1997 #text\_change 15-Sep-2000  
C/Accession: A54877  
R/Rainzliber, M.; Hasson, A.; Oren, R.; Burlingame, A.L.; Gordon, D.; Spira, M.E.; Zlot  
Biochemistry 33, 9523-9529, 1994  
A/Title: New mollusc-specific alpha-conotoxins block Ap15a neuronal acetylcholine release  
A/Reference number: A54877; MUID:94347719; PMID:8068627  
A/Accession: A54877  
A/Molecule type: protein  
A/Residues: 1-16 <PAI>  
R/Hu, S.H.; Gehrmann, J.; Guddat, L.W.; Alewood, P.F.; Craik, D.J.; Martin, J.L.  
submitted to the Brookhaven Protein Data Bank, January 1996  
A/Reference number: A66355; PDB:1BEN  
A/Contents: annotation; X-ray crystallography, 1.1 angstroms; residues 1-16  
C/Comment: This alpha-conotoxin, as an acetylcholine receptor inhibitor, is a postsynaptic neurotoxin  
C/Superfamily: alpha-conotoxin  
C/Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neurotoxin  
F/-8,3-16/Disulfide bonds: #status experimental  
F/16/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 39.0%; Score 48; DB 2; Length 16;  
Best Local Similarity 40.0%; Pred. No. 1.6;  
Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 5 CCLIPACRRNHKFC 19  
|||  
Db 2 CCCLPACRRNHKFC 16

RESULT 7  
T09220  
excyst complex protein sec5 - rat  
C/Species: Rattus norvegicus (Norway rat)  
C/Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 21-Jul-2000  
C/Accession: T09220  
R/Keen, Y.; Yoo, J.S.; Hazuka, C.D.; Peterson, K.E.; Hsu, S.C.; Scheller, R.H.  
Proc. Natl. Acad. Sci. U.S.A. 94, 14438-14443, 1997  
A/Title: Subunit structure of the mammalian excyst complex  
A/Reference number: Z16617; MUID:98070770; PMID:9405831  
A/Accession: T09220  
A/Status: translated from GB/EMBL/DBJ  
A/Molecule type: mRNA  
A/Residues: 1-924 <KEE>

A;Title: Selective expression of the high-affinity isoform of the folate receptor (FR-  
A;Reference number: S47554; MUID:94339186; PMID:8061055  
A;Accession: S47554  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-105 162-257 <PRA>  
R;Sadasiyan, E.; Rothenberg, S.P.  
J. Biol. Chem. 264, 5806-5811, 1989  
A;Title: The complete amino acid sequence of a human folate binding protein from KB cell  
A;Reference number: A32864; MUID:89174638; PMID:2538429  
A;Accession: A32864  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 24-183 'S', 185-249 <SA3>  
A;Cross-references: GB:M25317; NID:G182421; PIDN:AAA74896.1; PID:G182422  
R;Sadasiyan, E.; Rothenberg, S.P.  
Proc. Soc. Exp. Biol. Med. 189, 240-244, 1988  
A;Title: Molecular cloning of the complementary DNA for a human folate binding protein  
A;Reference number: A47570; MUID:89057954; PMID:3194438  
A;Accession: A47570  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 24-45 <SA2>  
A;Cross-references: EMBL:M35069; NID:G182419; PIDN:AAA35824.1; PID:G182420  
R;Juhrs, C.A.; Pittaraggon, P.; da Costa, M.; Rothenberg, S.P.; Slomiany, B.L.; Brink,  
Proc. Natl. Acad. Sci. U.S.A. 84, 6546-6549, 1987  
A;Title: Purified membrane and soluble folate binding proteins from cultured KB cells  
A;Reference number: A28316; MUID:87317689; PMID:3476960  
A;Accession: A28316  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 26-36, 'X', 38-43 <LUH>  
A;Experimental source: KB cells  
C;Genetics:  
A;Gene: GDB:FOLR1; FOLR  
A;Cross-references: GDB:128061; OMIM:136430  
A;Map position: 11q13.3-11q14.1  
C;Superfamily: folate-binding protein  
F;1-25/Domain: signal sequence #status predicted <SIG>  
F;26-257/Product: folate-binding protein #status predicted <MAT>  
F;31-257/Product: tumor-associated antigen #status experimental <ANT>

Query Match 38.2%; Score 47; DB 2; Length 257;  
Best Local Similarity 50.0%; Pred. No. 17;  
Matches 8; Conservative 3; Mismatches 3; Indels 2; Gaps 1;

QY 1 FNRCC--LIPACRRN 14  
||| | : |||:  
DB 84 FNNHCGEMAPACKEH 99

RESULT 9  
S29973  
protamine 1 - guinea pig  
C;Species: Cavia porcellus (guinea pig)  
C;Date: 12-Feb-1998 #sequence\_revision 20-Feb-1998 #text\_change 23-Jul-1999  
C;Accession: S29973; S29972  
R;Oliva, R.  
submitted to the EMBL Data Library, December 1991  
A;Reference number: S29972  
A;Accession: S29973  
A;Molecule type: DNA  
A;Residues: 1-48 <OLI>  
A;Cross-references: EMBL:Z11545; NID:949561; PIDN:CAA77644.1; PID:949562  
A;Accession: S29972  
A;Molecule type: mRNA  
A;Residues: 1-48 <OLW>  
A;Cross-references: EMBL:Z11544; NID:949563; PIDN:CAA77643.1; PID:949564  
C;Genetics:  
A;Introns: 35/1  
C;Superfamily: sperm histone  
C;Keywords: chromosomal protein; DNA binding; DNA condensation; nucleosome core; spermatogenesis

laxin 1 precursor - human

RESULT 14  
S59427  
hypothetical protein YDR220c - yeast (*Saccharomyces cerevisiae*)



A; Experimental source: strain H37Rv  
C; Gene: adhE2  
C; Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology  
F; 27-352/Domain: long-chain alcohol dehydrogenase homology <ADH>

Query Match 36.6%; Score 45; DB 2; Length 361;  
Best Local Similarity 40.0%; Pred. No. 43;  
Matches 8; Conservative 3; Mismatches 7; Indels 2; Gaps 1;

QY 2 NWR--CCLIPACRRNHKKFC 19  
||| ||| ||| |||  
DB 88 NNRVVGCGCRACKGRFRAYC 107

RESULT 17  
QRMSA1  
thyroid hormone receptor alpha-1 - mouse  
C; Species: Mus musculus (house mouse)  
C; Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 22-Jun-1999  
C; Accession: S14690; S08690  
R; Masuda, M.; Yasuhara, S.; Yamashita, M.; Shibuya, M.; Odaka, T.  
Nucleic Acids Res. 18, 3055, 1990  
A; Title: Nucleotide sequence of the murine thyroid hormone receptor (alpha-1) cDNA.  
A; Reference number: S14690; MUID: 90272421; PMID: 2349106  
A; Accession: S14690  
A; Status: translation not shown  
A; Molecule type: mRNA  
A; Residues: 1-410 <MAS>  
A; Cross-references: EMBL:X51983; NID: G50385; PIDN: CAA36241.1; PID: G50386  
C; Geneticks:  
A; Gene: erba-alpha  
C; Superfamily: thyroid hormone receptor; erba transforming protein homology  
C; Keywords: alternative splicing; DNA binding; proto-oncogene; thyroid hormone receptor  
F; 51-327/Domain: erba transforming protein homology <ERBA>  
F; 53-73/Region: zinc finger CCCC motif  
F; 91-115/Region: zinc finger CCCC motif  
F; 190-410/Domain: hormone binding #status Predicted <HRB>

Query Match 36.6%; Score 45; DB 1; Length 410;  
Best Local Similarity 46.7%; Pred. No. 47;  
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 5 CCLIPACRRNHKKFC 19  
||| ||| ||| |||  
DB 96 CCVIDKITRHHCLQC 110

RESULT 18  
E64503  
hypothetical protein MJ1631 - Methanococcus jannaschii  
C; Species: Methanococcus jannaschii  
C; Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 22-Oct-1999  
C; Accession: E64503  
R; Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, R.; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; Rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.  
Science 273, 1058-1073, 1996  
A; Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.R.  
A; Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii  
A; Reference number: A64300; MUID: 96337999; PMID: 8688087  
A; Accession: E64503  
A; Status: Preliminary; nucleic acid sequence not shown; translation not shown  
A; Molecule type: DNA  
A; Residues: 1-519 <BU>  
A; Cross-references: GB: U67603; GB: L77117; NID: G1592220; PIDN: AAB99652.1; PID: G1500530;  
C; Geneticks:  
A; Map position: FOR1611185-1612744

Query Match 36.6%; Score 45; DB 2; Length 519;  
Best Local Similarity 32.0%; Pred. No. 56;  
Matches 8; Conservative 4; Mismatches 7; Indels 6; Gaps 1;



MULT 21  
[518  
insposase Tam3 - garden snapdragon transposon Tam3  
Species: Antirrhinum majus (garden snapdragon)  
Date: 18-Feb-1994 #sequence\_revision 01-Dec-1995 #text\_change 21-Jul-2000  
Accession: S13518  
Mol. Biol. 16, 369-371, 1991  
Title: Structural analysis of Tam3, a transposable element from Antirrhinum majus, reveals a novel mechanism for transposition  
Reference number: S13518; MUID:91370883; PMID:1654157  
Accession: S13518  
Status: preliminary  
Molecule type: DNA  
Residues: 1-749 <HEH>  
Cross-references: EMBL:X55078; NID:g16063; PIDN:CAA38906.1; PID:g16064  
Genetics:  
Mobile element: transposon Tam3  
Superfamily: hypothetical transposase Ac9  
Query Match 36.6%; Score 45; DB 2; Length 749;  
Best Local Similarity 44.4%; Pred. No. 73;  
Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;  
2 NWRCCLIPACRRNHKKFC 19  
|||  
142 NWAQCLLCPTRYSHKTCG 159  
|||  
MULT 22  
[518  
arm histone - sheep  
Alternate names: cysteine-rich protamine; protamine  
Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
Date: 04-Dec-1986 #sequence\_revision 04-Dec-1986 #text\_change 05-Sep-1997  
Accession: A02658  
Mol. Biol. 144, 121-125, 1984  
Title: Primary structure of the ram (Ovis aries) protamine.  
Reference number: A02658; MUID:85003651; PMID:6479168  
Accession: A02658  
Molecule type: protein  
Residues: 1-50 <SAU>  
Superfamily: sperm histone  
Keywords: chromosomal protein; DNA binding; nucleosome core; spermatogenesis  
Disulfide bonds: interchain (to 22) #status predicted  
5-14, 39-47/Disulfide bonds: #status predicted  
22/Disulfide bonds: interchain (to 5) #status predicted  
38/Disulfide bonds: interchain #status predicted  
Query Match 36.2%; Score 44.5; DB 1; Length 50;  
Best Local Similarity 40.0%; Pred. No. 12;  
Matches 8; Conservative 4; Mismatches 5; Indels 3; Gaps 1;  
3 WRCCCLIPA---CRNHKKFC 19  
:|||||:|||||:  
3 YRCCLTHSGRCRRRRRC 22  
|||  
MULT 23  
[518  
arm histone P1 - bovine  
Alternate names: arginine-rich protamine; cysteine-rich protamine; protamine P1; sperm  
Species: Bos primigenius taurus (cattle)  
Date: 24-Apr-1984 #sequence\_revision 30-Jun-1992 #text\_change 22-Jun-1999  
Accession: A29911; A26450; A26041; A24375; A61342  
Kravetz, S.A.; Connor, W.; Dixon, G.H.  
Mol. Chem. 263, 321-326, 1988  
Title: Bovine protamine genes contain a single intron. The structures of the two alleles are compared  
Reference number: A29911; MUID:88087109; PMID:3335501  
Accession: A29911  
Molecule type: DNA  
Residues: 1-51 <KTA>  
Cross-references: GB:M18396; NID:g163619; PIDN:AAA30735.1; PID:g163620

R;Kravetz, S.A.; Connor, W.; Dixon, G.H.  
DNA 6, 47-57, 1987  
A>Title: Cloning of bovine P1 protamine cDNA and the evolution of vertebrate P1 protami  
A'Reference number: A26450; MUID:87161234; PMID:3829889  
A'Accession: A26450  
A'Molecule type: mRNA  
A'Residues: 1-51 <KR2>  
A'Cross-references: GB:M14559; NID:g163632; PIDN:AAA30741.1; PID:g163633  
R;Lee, C.H.; Mansouri, A.; Hecht, W.; Hecht, N.B.; Engel, W.  
Mol. Chem. Hoppe-Seyler 368, 131-135, 1987  
A>Title: Nucleotide sequence of a bovine protamine cDNA.  
A'Reference number: A26041; MUID:87184911; PMID:2436637  
A'Accession: A26041  
A'Molecule type: mRNA  
A'Residues: 2-51 <LEB>  
A'Cross-references: GB:M18625  
A>Note: the codon for residue 30-Phe is shown as TCT  
R;Mazrimas, J.A.; Corzett, M.; Campos, C.; Balhorn, R.  
Biochim. Biophys. Acta 872, 11-15, 1986  
A>Title: A corrected primary sequence for bull protamine.  
A'Reference number: A24375; MUID:86269888; PMID:3730390  
A'Accession: A24375  
A'Molecule type: protein  
A'Residues: 2-51 <MAZ>  
R;Cooling, J.P.; Monfoort, C.H.; Rozijn, T.H.; Leuven, J.A.G.; Schiphof, R.; Steyn-Par  
Biochim. Biophys. Acta 285, 1-14, 1972  
A>Title: The complete amino acid sequence of the basic nuclear protein of bull spermato  
A'Reference number: A61342; MUID:73124384; PMID:4675900  
A'Accession: A61342  
A'Molecule type: protein  
A'Residues: 2-39/43-51 <COE>  
R;Balhorn, R.; Corzett, M.; Mazrimas, J.; Watkins, B.  
Biochemistry 30, 175-181, 1991  
A>Title: Identification of bull protamine disulfides.  
A'Reference number: A37137; MUID:91105078; PMID:1988019  
A'Contents: annotation: disulfide bonds  
C:Genetics:  
A:Introns: 38/1  
C:Function:  
A>Description: binds to and packages sperm DNA in a condensed form of chromatin that is  
C:Superfamily: sperm histone  
C:Keywords: chromosomal protein; DNA binding; nucleosome core; spermatogenesis  
F:2-51/Product: protamine P1 #status experimental <MAR>  
F:6/Disulfide bonds: interchain (to 23) #status experimental  
F:7-15, 40-48/Disulfide bonds: #status experimental  
F:23/Disulfide bonds: interchain (to 6) #status experimental  
F:39/Disulfide bonds: interchain #status experimental  
Query Match 36.2%; Score 44.5; DB 1; Length 51;  
Best Local Similarity 40.0%; Pred. No. 12;  
Matches 8; Conservative 4; Mismatches 5; Indels 3; Gaps 1;  
QY 3 WRCCCLIPA---CRNHKKFC 19  
:|||||:|||||:  
Db 4 YRCCLTHSGRCRRRRRC 23  
|||  
RESULT 24  
[518  
A60603  
N/AAlternate names: aldose reductase  
C:Species: Rattus norvegicus (Norway rat)  
C>Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 20-Apr-2000  
C'Accession: A60603; S00079; B60603; I53649  
R;Carper, D.A.; Wistow, G.; Nishimura, C.; Graham, C.; Watanabe, K.; Fujii, Y.; Hayashi  
Exp. Eye Res. 49, 377-388, 1989  
A>Title: A superfamily of NADPH-dependent reductases in eukaryotes and prokaryotes.  
A'Reference number: A60603; MUID:90005742; PMID:2507340  
A'Accession: A60603  
A>Status: not compared with conceptual translation  
A'Molecule type: mRNA  
A'Residues: 1-316 <CAR>  
R;Carper, D.; Nishimura, C.; Shinohara, T.; Dietzhold, B.; Wistow, G.; Craft, C.; Kado

3S Lett. 220, 209-213, 1987  
Title: Aldose reductase and rho-crystallin belong to the same protein superfamily as a reference number: S00079; MUID:87276556; PMID:3111886  
Accession: S00079  
Molecule type: mRNA  
Residues: 33-316 <CA2>  
Cross-references: EMBL:X05884  
Note: 45-Ser and 54-Trp were also found  
Accession: B60603  
Molecule type: protein  
Residues: 34-60, 'XX', 92-108, 146-173, 204-231, 244-252, 276-294 <CA3>  
Note: Part of this sequence was confirmed by protein sequencing  
Braham, C.E.; Szpirer, C.; Levan, G.; Carper, D.  
Title: Characterization of the aldose reductase-encoding gene family in rat.  
Reference number: I53649; MUID:92084118; PMID:1748296  
Accession: I53649  
Status: translated from GB/EMBL/DBJ  
Molecule type: DNA  
Residues: 1-316 <RES>  
Cross-references: GB:M60322; NID:g202851; PIDN:AAA0721.1; PID:g202852  
Comment: Aldose reductase catalyzes reduction of a variety of sugars to sugar alcohols  
Comment: This enzyme is active in the eye lens, where an accumulation of sugar alcohol  
Genetics:  
Introns: 22/3; 78/3; 117/3; 143/3; 184/3; 220/2; 247/3; 275/3; 303/2  
Superfamily: aldehyde reductase  
Keywords: eye lens; NADP; oxidoreductase  
263/Active site: Lys #status predicted  
Query Match 36.2%; Score 44.5; DB 1; Length 316;  
Best Local Similarity 41.2%; Pred. No. 46;  
Matches 7; Conservative 4; Mismatches 5; Indels 1; Gaps 1;  
2 NWRCLIPACRRNHKPF 18  
|||||:|:|:  
295 NWRVCAIMSCAK-HKDY 310  
SULT 25  
9484  
aldehyde reductase (EC 1.1.1.21) - mouse  
Species: Mus musculus (house mouse)  
Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 21-Jul-2000  
Accession: I49484  
Gui, T.; Tanimoto, T.; Kokai, Y.; Nishimura, C.  
Title: Presence of a closely related subgroup in the aldo-ketoreductase family of the  
Reference number: I49484; MUID:95154325; PMID:7851421  
Accession: I49484  
Status: preliminary; translated from GB/EMBL/DBJ  
Molecule type: mRNA  
Residues: 1-316 <RES>  
Cross-references: GB:D32250; NID:g1384073; PIDN:BAA06980.1; PID:g786001  
Superfamily: aldehyde reductase  
Keywords: NADP; oxidoreductase  
Query Match 36.2%; Score 44.5; DB 2; Length 316;  
Best Local Similarity 41.2%; Pred. No. 46;  
Matches 7; Conservative 4; Mismatches 5; Indels 1; Gaps 1;  
2 NWRCLIPACRRNHKPF 18  
|||||:|:|:  
295 NWRVCAIMSCAK-HKDY 310  
SULT 26  
8279  
ultradrug resistance transport protein - slime mold (Dictyostelium discoideum)  
Species: Dictyostelium discoideum  
Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
Accession: T18279  
Shaulsky, G.; Joomis, W.F.  
Submitted to the EMBL Data Library, June 1996

A:Reference number: Z18855  
A:Accession: T18279  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-1743 <SHA>  
A:Cross-references: EMBL:U60086; NID:g1399914; PID:g1399915; PIDN:AA803331.1  
C:Genetics:  
A:Gene: tagC  
Query Match 36.2%; Score 44.5; DB 2; Length 1743;  
Best Local Similarity 40.9%; Pred. No. 1.6e+02;  
Matches 9; Conservative 2; Mismatches 6; Indels 5; Gaps 1;  
QY 3 WRCCLIPACRRNH-----KKFC 19  
DB 933 WSSCLIQSCDNNYNSIKKRC 954  
RESULT 27  
T24864  
hypothetical protein T12D8.1 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 29-Oct-1999  
C:Accession: T24864; T27892  
R:McMurray, A.  
Submitted to the EMBL Data Library, October 1996  
A:Reference number: Z19944  
A:Accession: T24864  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-2561 <WIL>  
A:Cross-references: EMBL:Z81120; PIDN:CAB03348.1; GSPDB:GN00021; CBSP:T12D8.1  
A:Experimental source: clone T12D8  
R:Steward, C.  
Submitted to the EMBL Data Library, November 1996  
A:Reference number: Z20436  
A:Accession: T27892  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-2561 <WI2>  
A:Cross-references: EMBL:Z82094; PIDN:CAB05024.1; GSPDB:GN00021; CBSP:T12D8.1  
A:Experimental source: clone ZK525  
C:Genetics:  
A:Gene: CBSP:T12D8.1  
A:Map position: 3  
A:Introns: 44/3; 78/3; 104/2; 251/2; 466/3; 504/3; 548/3; 662/2; 747/1; 962/1; 1355/3;  
Query Match 36.2%; Score 44.5; DB 2; Length 2561;  
Best Local Similarity 60.0%; Pred. No. 2.1e+02;  
Matches 9; Conservative 0; Mismatches 5; Indels 1; Gaps 1;  
QY 3 WRCCLIPACRR-NHK 16  
DB 605 WRQWCSCRRCRCHK 619  
RESULT 28  
A59046  
alpha-conotoxin MII - cone shell (Conus magus)  
C:Species: Conus magus (magus cone)  
C:Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 16-Jul-1999  
C:Accession: A59046  
R:Cartier, G.E.; Yoshikami, D.; Gray, W.R.; Luo, S.; Olivera, B.M.; McIntosh, J.M.  
J. Biol. Chem. 271, 7522-7528, 1996  
A:Title: A new alpha-conotoxin which targets alpha3beta2 nicotinic acetylcholine receptor  
A:Reference number: A59046; MUID:96205934; PMID:8631783  
A:Accession: A59046  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-16 <CAR>  
C:Superfamily: alpha-conotoxin  
C:Keywords: acetylcholine receptor inhibitor; amidated carboxyl end, postsynaptic neuro  
F;1-16/Product: alpha-conotoxin MII #status experimental <MAI>

1-8,3-16/Disulfide bonds: #status experimental  
 16/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 35.8%; Score 44; DB 2; Length 16;  
 Best Local Similarity 40.0%; Pred. No. 6.1;  
 Matches 6; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

5 CCLIPACRRNHKKFC 19  
 |||||  
 2 CCNPFVCHLSNLC 16

SULT 29  
 3042

cha-conotoxin Epi - cone shell (Conus episcopatus)  
 Species: Conus episcopatus (bishop's cone)  
 Date: 23-Jul-1999 #sequence\_revision 23-Jul-1999 #text\_change 13-Aug-1999  
 Accession: A59042

Loughnan, M.; Bond, T.; Atkins, A.; Cuevas, J.; Adams, D.J.; Broxton, N.M.; Livett, B.  
 Biol. Chem. 273, 15667-15674, 1998

Title: Alpha-conotoxin Epi, a novel sulfated peptide from Conus episcopatus that selected  
 reference number: A59042; MUID:98288307; PMID:9624161

Accession: A59042  
 Status: preliminary  
 Molecule type: protein  
 Residues: 1-16 <LOU>

Superfamily: alpha-conotoxin  
 Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; post-synaptic neuro  
 1-16/Product: alpha-conotoxin Epi #status experimental <MAP>  
 1-8,3-16/Disulfide bonds: #status experimental  
 15/Binding site: sulfate (Tyr) (covalent) #status experimental  
 16/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 35.8%; Score 44; DB 2; Length 16;  
 Best Local Similarity 40.0%; Pred. No. 6.1;  
 Matches 6; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

5 CCLIPACRRNHKKFC 19  
 |||||  
 2 CCSDPRCNRNPDYC 16

SULT 30  
 7745

xx prenyl proteinase 2 - fission yeast (Schizosaccharomyces pombe)  
 Species: Schizosaccharomyces pombe  
 Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 07-Dec-1999  
 Accession: T37745

Medler, H.; Wambutt, R.; Wood, V.; Rajandream, M.A.; Barrell, B.G.  
 Submitted to the EMBL Data Library, December 1998  
 Reference number: Z21744  
 Accession: T37745

Status: preliminary; translated from GB/EMBL/DBDJ  
 Molecule type: DNA  
 Residues: 1-271 <WED>  
 Cross-references: EMBL:AL035064; PIDN:CAA22596.1; GSPDB:GN00066; SPDB:SPAC1697.02  
 Experimental source: strain 972h-; cosmid c1687  
 Genetics:  
 Gene: SPDB:SPAC1697.02  
 Map position: 1  
 Introns: 121/3

Query Match 35.8%; Score 44; DB 2; Length 271;  
 Best Local Similarity 55.6%; Pred. No. 48;  
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

3 WRCCLPAC 11  
 :|||:  
 130 FRCCIVPIC 138

SULT 31  
 3440

aldose reductase homolog - mouse  
 C:Species: Mus musculus (house mouse)  
 C>Date: 19-May-1995 #sequence\_revision 19-May-1995 #text\_change 11-Jun-1999  
 C:Accession: A53440

R:Donohue, P.J.; Alberts, G.F.; Hampton, B.S.; Winkles, J.A.  
 J. Biol. Chem. 269, 8604-8609, 1994

A>Title: A delayed-early gene activated by fibroblast growth factor-1 encodes a protein  
 A:Reference number: A53440; MUID:94179253; PMID:7510692

A:Accession: A53440  
 A>Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-316 <DON>  
 A:Cross-references: GB:U04204; NID:G463376; PIDN:AAA16953.1; PID:G463377  
 C:Superfamily: aldehyde reductase

Query Match 35.8%; Score 44; DB 2; Length 316;  
 Best Local Similarity 75.0%; Pred. No. 54;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 NWRCLIP 9  
 |||||  
 DB 295 NWRACLLP 302

RESULT 32  
 T23090

hypothetical protein H13N06.6 - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 18-Feb-2000  
 C:Accession: T23090

R:Lennard, N.  
 submitted to the EMBL Data Library, October 1997

A:Reference number: Z19673  
 A:Accession: T23090  
 A>Status: preliminary; translated from GB/EMBL/DBDJ  
 A:Molecule type: DNA  
 A:Residues: 1-633 <WIL>  
 A:Cross-references: EMBL:Z99942; PIDN:CAB17071.1; GSPDB:GN00028; CESP:H13N06.6  
 A:Experimental source: clone H13N06  
 C:Genetics:  
 A:Gene: CESP:H13N06.6  
 A:Map position: X  
 A:Introns: 134/3; 179/3; 206/3; 381/2; 420/3; 541/2

Query Match 35.8%; Score 44; DB 2; Length 633;  
 Best Local Similarity 61.5%; Pred. No. 90;  
 Matches 8; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

QY 3 WRCCLPACRRNH 15  
 |||||  
 DB 50 WRCC--PRWRGNH 60

RESULT 33  
 A34406

aldehyde reductase (EC 1.1.1.21) - rabbit (fragment)  
 C:Species: Oryctolagus cuniculus (domestic rabbit)  
 C>Date: 22-Jun-1990 #sequence\_revision 22-Jun-1990 #text\_change 11-Jun-1999  
 C:Accession: A34406

R:Garcia-Perez, A.; Martin, B.; Murphy, H.R.; Uchida, S.; Murer, H.; Cowley Jr., B.D.;  
 J. Biol. Chem. 264, 16815-16821, 1989

A>Title: Molecular cloning of cDNA coding for kidney aldose reductase. Regulation of sp  
 A:Reference number: A34406; MUID:89380313; PMID:2506183

A:Accession: A34406  
 A>Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-302 <GAR>  
 A:Cross-references: GB:J05048; NID:G164756; PIDN:AAA31157.1; PID:G164757  
 C:Superfamily: aldehyde reductase  
 C:Keywords: oxidoreductase

Query Match 35.4%; Score 43.5; DB 2; Length 302;  
 Best Local Similarity 41.2%; Pred. No. 62;

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A,Cross-references: EMBL:ALC31583; NID:e1321005; PID:e1330107; PIDN:CAR20903.1
C:Genetics:
A:Gene: FlyBase:Rbf
A,Cross-references: FlyBase:FBgn0015799
A,Introns: 63/3; 110/2; 173/2; 291/3; 402/2; 647/3; 774/3
Query Match          35.4%; Score 43.5; DB 2; Length 845;
Best Local Similarity 61.5%; Pred. No. 1.3e+02;
Matches      8; Conservative    1; Mismatches   3; Indels     1; Gaps      1;
```

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

protein - protein search, using sw model

on: February 18, 2004, 06:03:18 ; Search time 47 Seconds  
(without alignments)  
21.050 Million cell updates/sec

le: US-09-806-376-1

fect score: 123

quence: 1 FNRWCCCLIPACRRNHKKFC 19

ring table: BUCSUM62

Gapop 10.0 , Gapext 0.5

urched: 141681 seqs, 52070155 residues

al number of hits satisfying chosen parameters: 141681

imum DB seq length: 0

imum DB seq length: 2000000000

it-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

abase : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

ult No.	Score	Query Match	Length	ID	Description
1	123	100.0	19	1 CXR CONTU	P58811 conus tulip
2	49	39.8	67	1 IBB2 SEIT	P19860 setaria ita
3	49	39.8	67	1 IBB3 SEIT	P22737 setaria ita
4	48	39.0	16	1 CXAA CONTE	P50984 conus penna
5	48	39.0	66	1 CXA2 CONTE	Q9xzk7 conus texti
6	48	39.0	924	1 SEC5 MOUSE	Q9ddh1 mus musculus
7	48	39.0	924	1 SEC5 RAT	O54921 rattus norv
8	47	38.2	257	1 FOLL1 HUMAN	P15328 homo sapien
9	46.5	37.8	47	1 HSP11 CAVPO	P35304 cavia porce
10	46	37.4	185	1 RELL1 HUMAN	P04808 homo sapien
11	45.5	37.0	222	1 WED1 CHICK	Q8J933 gallus gall
12	45	36.6	64	1 IBB1 COILA	P07679 coix lachry
13	45	36.6	69	1 CXA1 CONTE	Q9xzk6 conus texti
14	45	36.6	519	1 YG31 METJA	Q59025 methanococc
15	45	36.6	593	1 GRN HUMAN	P28799 h granulin
16	44.5	36.2	50	1 HSP1 BOVIN	P02318 bos taurus
17	44.5	36.2	50	1 HSP1 SHEEP	P04102 ovis aries
18	44.5	36.2	315	1 ALDR MOUSE	P45376 mus musculus
19	44.5	36.2	315	1 ALDR RAT	P07943 rattus norv
20	44.5	36.2	1743	1 TAGC DICDI	Q23868 dictyosteli
21	44	35.8	16	1 CXA1 CONEP	P56638 conus epis
22	44	35.8	16	1 CXA2 CONNA	P56636 conus magus
23	44	35.8	271	1 RCEL1 SCHPO	Q94448 schizosacch
24	44	35.8	315	1 ALD2 MOUSE	P45377 mus musculus
25	44	35.8	360	1 FADH ANTHE	P80094 amycolotops
26	44	35.8	924	1 SEC5 HUMAN	Q96kpl homo sapien
27	43.5	35.4	315	1 ALDR PIG	P80276 sus scrofa
28	43.5	35.4	315	1 ALDR RABIT	P15122 crotolagus
29	43.5	35.4	797	1 RBF DROME	Q24472 drosophila
30	43.5	35.4	1218	1 JAG1 HUMAN	P78504 homo sapien
31	43	35.0	128	1 ACPS BUCBP	P59475 bucmerna ap
32	43	35.0	222	1 FOLL1 BOVIN	P02702 bos taurus
33	43	35.0	249	1 YAT6 HOBL	P05449 rhodopseudo

34	43	35.0	255	1 FOL2 HUMAN	P14207 homo sapien
35	43	35.0	678	1 CG15 ARATH	Q9sl29 arabidopsis
36	43	35.0	1961	1 MYH9 RAT	Q62812 rattus norv
37	42.5	34.6	315	1 ALDR HUMAN	P15121 homo sapien
38	42.5	34.6	612	1 UNC5 CABEL	P34710 caenorabdi
39	42.5	34.6	1218	1 JAG1 MOUSE	Q9gxx0 mus musculus
40	42	34.1	16	1 CXAB CONPE	P50985 conus penna
41	42	34.1	365	1 P43 XENLA	P25456 xenopus lae
42	42	34.1	452	1 KRMI XENLA	Q90y90 xenopus lae
43	42	34.1	473	1 KRMI MOUSE	Q9n43 mus musculus
44	42	34.1	473	1 KRMI RAT	Q92484 rattus norv
45	42	34.1	475	1 KRMI HUMAN	Q96mu8 homo sapien
46	42	34.1	588	1 GRN RAT	P23785 r granulin
47	42	34.1	607	1 ELM3 HUMAN	Q86yz7 mus musculus
48	42	34.1	671	1 ELM3 MOUSE	P16144 homo sapien
49	42	34.1	1822	1 ITB4 HUMAN	P49867 bombyx mori
50	41.5	33.7	555	1 FTF1 BOMMO	

ALIGNMENTS

RESULT 1  
CXR CONTU STANDARD; PRT; 19 AA.  
ID P58811: 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Rho-conotoxin T1A (Rho-T1A)  
OS Conus tulipa (fish-hunting cone snail) (Tulip cone).  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;  
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hyposogastropoda;  
OC Neogastropoda; Conoidea; Conidae; Conus.  
OX NCBI\_taxid=8495;  
RN [1]  
RP SEQUENCE, SYNTHESIS, AND STRUCTURE BY NMR.  
RC TISSUE=Venom;  
RX MEDLINE=21419681; PubMed=11528421;  
RA Sharpe I.A., Gehrmann J., Loughnan M.L., Thomas L., Adams D.A.,  
RA Atkins A., Falant E., Craik D.J., Adams D.J., Alewood P.F.,  
RA Lewis R.V.;  
RT "Two new classes of conopeptides inhibit the alpha-adrenoceptor and  
RT noradrenaline transporter.";  
RL Nat. Neurosci. 4:902-907(2001).  
CC -!- FUNCTION: Inhibits alpha-1 adrenergic receptors.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.  
CC -!- MASS SPECTROMETRY: MW=2390.15; METHOD=Electrospray.  
CC -!- SIMILARITY: Belongs to the rho-conotoxin family.  
DR PDB; ILEN; 03-APR-02.  
KW Toxin; Amidation; 3D-structure.  
FT DISULFID 5 11  
FT MOD\_RES 6 19  
FT TURN 12 3  
FT TURN 13 14  
FT TURN 16 19  
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IBB2_SETIT STANDARD; PRT; 67 AA.
PI9860;
01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Bowman-Birk type major trypsin inhibitor (PMTI-II).
Setaria italica (Foxtail millet).
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
PACCAD clade; Panicoideae; Paniceae; Setaria.
NCBI_TaxID=4555;
[1]
SEQUENCE.
MEDLINE=91154179; PubMed=2292595;
Tashiro M., Asao T., Hirata C., Takahashi K., Kanamori M.;
"The complete amino acid sequence of a major trypsin inhibitor from
seeds of foxtail millet (Setaria italica).";
J. Biochem. 108:669-672(1990).
-|- SIMILARITY: Belongs to the Bowman-Birk serine protease inhibitor
family.
PIR; JX0136; TILF2.
HSSP; P56679; IPBI.
InterPro; IPR000877; Bowman-Birk_leg.
Pfam; PF00228; Bowman-Birk_leg; 2.
ProDom; PD002168; Bowman-Birk_leg; 1.
SMART; SM00269; BowB; 1.
PROSITE; PS00281; BOWMAN_BIRK; 1.
Serine protease inhibitor.
ACT_SITE 16 17 INTERACTION WITH TRYPSIN (BY SIMILARITY).
DISULFID 8 63 BY SIMILARITY.
DISULFID 9 24 BY SIMILARITY.
DISULFID 14 22 BY SIMILARITY.
DISULFID 31 38 BY SIMILARITY.
DISULFID 35 51 BY SIMILARITY.
SEQUENCE 67 AA; 7679 MW; 109AF30F33248949 CRC64;

Query Match 39.8%; Score 49; DB 1; Length 67;
Best Local Similarity 35.3%; Pred. No. 0.73;
Matches 6; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

3 WRCCCLIPACRRNHKFC 19
6 WKCCDLQCTKTSIPAPC 22

SULT 3
IBB3_SETIT STANDARD; PRT; 67 AA.
P22737;
01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Bowman-Birk type trypsin inhibitor III (PMTI-III).
Setaria italica (Foxtail millet).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
PACCAD clade; Panicoideae; Paniceae; Setaria.
NCBI_TaxID=4555;
[1]
SEQUENCE.
MEDLINE=91299279; PubMed=1368693;
Tashiro M., Asao T., Hirata C., Takahashi K.;
"Purification, characterization, and amino acid sequence of foxtail
millet trypsin inhibitor III.";
Agric. Biol. Chem. 55:419-426(1991).
-|- SIMILARITY: Belongs to the Bowman-Birk serine protease inhibitor
family.
PIR; JG0013; TILF3.
HSSP; P56679; IPBI.
InterPro; IPR000877; Bowman-Birk_leg.
Pfam; PF00228; Bowman-Birk_leg; 2.
ProDom; PD002168; Bowman-Birk_leg; 1.
SMART; SM00269; BowB; 1.

DR PROSITE; PS00281; BOWMAN_BIRK; 1.
KW Serine protease inhibitor.
FT ACT_SITE 16 17 INTERACTION WITH TRYPSIN (BY SIMILARITY).
FT DISULFID 8 63 BY SIMILARITY.
FT DISULFID 9 24 BY SIMILARITY.
FT DISULFID 14 22 BY SIMILARITY.
FT DISULFID 31 38 BY SIMILARITY.
FT DISULFID 35 51 BY SIMILARITY.
SQ SEQUENCE 67 AA; 7680 MW; 0D5AF30F33248949 CRC64;

Query Match 39.8%; Score 49; DB 1; Length 67;
Best Local Similarity 35.3%; Pred. No. 0.73;
Matches 6; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

OY 3 WRCCCLIPACRRNHKFC 19
DB 6 WKCCDLQCTKTSIPAPC 22

RESULT 4
CXAA_CONPE STANDARD; PRT; 16 AA.
ID CXAA_CONPE
AC P50984;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Alpha-conotoxin Pn1A.
OS Conus pennaceus (Feathered cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=37335;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=94347719; PubMed=8068627;
RA Fainzilber M., Hasson A., Oren R., Burlingame A.L., Gordon D.,
RA Spira M.E., Zlotkin E.;
RT "New mollusc-specific alpha-conotoxins block Aplysia neuronal
acetylcholine receptors.";
RL Biochemistry 33:9523-9529(1994).
RN [2]
RP SULFATION OF TYR-15.
RX MEDLINE=99242956; PubMed=10226369;
RA Wolfender J.L., Chu F., Ball H., Wolfender F., Fainzilber M.,
RA Baldwin M.A., Burlingame A.L.;
RT "Identification of tyrosine sulfation in Conus pennaceus conotoxins
alpha-Pn1A and alpha-Pn1B: further investigation of labile sulfo- and
phosphopeptides by electrospray, matrix-assisted laser
desorption/ionization (MALDI) and atmospheric pressure MALDI mass
spectrometry.";
RL J. Mass Spectrom. 34:447-454(1999).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (1.1 ANGSTROMS).
RX MEDLINE=96311277; PubMed=8740364;
RA Hu S.-H., Gehrmann J., Guddat L.W., Alewood P.F., Craik D.J.,
RA Martin J.L.;
RT "The 1.1 A crystal structure of the neuronal acetylcholine receptor
antagonist, alpha-conotoxin Pn1A from Conus pennaceus.";
RL Structure 4:417-423(1996).
CC -|- FUNCTION: Alpha-conotoxins act on postsynaptic membranes, they
bind to the nicotinic acetylcholine receptors (nAChR) and thus
inhibit them. In contrast to other alpha-conotoxins, which are
selective for vertebrate skeletal muscle nAChR, the Conus
pennaceus alpha-conotoxins block nAChR in mollusks.
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -|- SIMILARITY: Belongs to the conotoxin A-superfamily. Alpha-type
family.
PIR; A54877; A54877.
PDB; 1PEN; 21-APR-97.
KW Postsynaptic neurotoxin; Neurotoxin; Toxin;
Acetylcholine receptor inhibitor; Amidation; Sulfation; 3D-structure.

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DISULFID 2 8  
 DISULFID 3 16  
 MOD\_RES 15 15  
 MOD\_RES 16 16  
 HELIX 2 4  
 HELIX 6 11  
 TURN 13 16  
 SEQUENCE 16 AA; 1628 MW; 05310FF95EC99005 CRC64;  
 Query Match 39.0%; Score 48; DB 1; Length 16;  
 best Local Similarity 40.0%; Pred. No. 0.26;  
 Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;  
 5 CCLIPACRRNHKKFC 19  
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 2 CCSLPFCAANNPDYC 16

MULT 5  
 12 CONTE CONTE STANDARD; PRT; 66 AA.  
 Q9XZK7;  
 16-OCT-2001 (Rel. 40, Created)  
 16-OCT-2001 (Rel. 40, Last sequence update)  
 28-FEB-2003 (Rel. 41, Last annotation update)  
 Alpha-type conotoxin Tx2 precursor.  
 Conus textile (Cloth-of-gold cone).  
 Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;  
 Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;  
 Neogastropoda; Conoidea; Conidae; Conus.  
 NCBI TaxID=6494;  
 [1]  
 SEQUENCE FROM N.A.  
 TISSUE=Venom duct;  
 MEDLINE=20037955; PubMed=10573284;  
 Lu B.-S., Yu F., Zhao D., Huang P.-T., Huang C.-F.;  
 "Conopeptides from *Conus striatus* and *Conus textile* by cDNA  
 cloning."  
 Peptides 20:1139-1144 (1999).  
 FUNCTION: Alpha-conotoxins act on postsynaptic membranes, they  
 bind to the nicotinic acetylcholine receptors (nAChR) and thus  
 inhibit them (By similarity).  
 SUBCELLULAR LOCATION: Secreted.  
 TISSUE SPECIFICITY: Expressed by the venom duct.  
 SIMILARITY: Belongs to the conotoxin A-superfamily. Alpha-type  
 family.

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EMBL; AF146353; AAC31913.1; -  
 Postsynaptic neurotoxin; Neurotoxin; Toxin;  
 Acetylcholine receptor inhibitor; Signal.  
 SIGNAL 1 21  
 POTENTIAL.  
 PROPEP 22 49  
 BY SIMILARITY.  
 PEPTIDE 50 66  
 ALPHA-TYPE CONOTOXIN TX2.  
 DISULFID 51 57  
 BY SIMILARITY.  
 DISULFID 52 65  
 BY SIMILARITY.  
 SEQUENCE 66 AA; 7254 MW; EDD859BBA394F26F CRC64;

Query Match 39.0%; Score 48; DB 1; Length 66;  
 best Local Similarity 46.7%; Pred. No. 1;  
 Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;  
 5 CCLIPACRRNHKKFC 19  
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 51 CCSHPACNVDPHC 65

RESULT 6  
 SECS\_MOUSE  
 ID SECS\_MOUSE STANDARD; PRT; 924 AA.  
 AC Q9D4HL;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Exocyst complex component Sec5.  
 SECS OR SECS1.  
 GN SECS OR SECS1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Testis;  
 EX MEDLINE=22354683; PubMed=12466851;  
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
 RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,  
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojibori T.,  
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
 RA Schrim L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,  
 RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,  
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,  
 RA Gasterland T., Gariboldi M., Gliss C., Godzik A., Gough J.,  
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,  
 RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,  
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,  
 RA Maglott D.R., Maltais L., Marchionni L., McKensie L., Miki H.,  
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,  
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 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,  
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
 RA Birney E., Hayashizaki Y.;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 60,770 full-length cDNAs."  
 RL Nature 420:563-573 (2002).  
 [2]  
 SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6; TISSUE=Brain;  
 EX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
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 RA Fahey J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzyzinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences."  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 [3]  
 STRUCTURE BY NMR OF RALA-BINDING DOMAIN.





```

NCBI_TaxID=10141;
[1] _SEQUENCE FROM N.A.
STRAIN=JML09;
Queralt R., Adroer R., Oliva R.;
Submitted (DEC-1991) to the EMBL/GenBank/DBJ databases.
-!- FUNCTION: Protamines substitute for histones in the chromatin of
sperm during the haploid phase of spermatogenesis. They compact
sperm DNA into a highly condensed, stable and inactive complex.
-!- SUBUNIT: Cross-linked by interchain disulfide bonds around the
DNA-helix.
-!- SUBCELLULAR LOCATION: Nuclear.
-!- TISSUE SPECIFICITY: Testis.
-!- SIMILARITY: Belongs to the protamine P1 family.
-----
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-----
EMBL; M83896; AAA58349.1; -
EMBL; Z11544; CAA77643.1; -
EMBL; Z11545; CAA77644.1; -
PIR; S29973; S29973.
InterPro; IPR000221; Protamine P1.
Pfam; PF00260; protamine P1; 1.
PROSITE; PS00048; NUCLEOSOME CORE; Spermatogenesis; DNA-binding;
Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding;
Testis; DNA condensation; Nuclear protein.
INIT MET 0 BY SIMILARITY.
SEQUENCE 47 AA; 6553 MW; D937107E37DE704D CRC64;
Query Match 37.8%; Score 46.5; DB 1; Length 47;
Best Local Similarity 42.1%; Pred. No. 1.2;
Matches 8; Conservative 4; Mismatches 4; Indels 3; Gaps 1;
3 WRCCLIPA---CRNKKX 18
:|||||:|||||:
3 YRCRSPGSRCKRRRRRP 21

SULT 10
[1] HUMAN
RELL_HUMAN STANDARD; PRT; 185 AA.
P04808; Q99936; Q9UQJ1;
13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Prorelaxin H1 precursor.
RLN1.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE=85051298; PubMed=6548702;
Hudson P., John M., Crawford R., Haralambidis J., Scanlon D.,
Gorman J., Tregear G., Shine J., Niall H.;
"Relaxin gene expression in human ovaries and the predicted structure
of a human preprorelaxin by analysis of cDNA clones."
EMBO J. 3:2333-2339(1984).
[2]
SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE=83141755; PubMed=6298628;
Hudson P., Haley J., John M., Cronk M., Crawford R., Haralambidis J.,
Tregear G., Shine J., Niall H.;
"Structure of a genomic clone encoding biologically active human
relaxin."
Nature 301:628-631(1983).

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RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RA Serra H.; (AUG-2000) to the EMBL/GenBank/DBJ databases.
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Prostate;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
Raba S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield V.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences."
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RP PARTIAL SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND TISSUE
SPECIFICITY.
RC TISSUE=Prostate;
RX MEDLINE=96328899; PubMed=8735594;
RA Gunnersen J.M., Fu P., Roche P.J., Tregear G.W.;
"Expression of human relaxin genes: characterization of a novel
alternatively-spliced human relaxin mRNA species."
Mol. Cell. Endocrinol. 118:85-94(1996).
RN [6]
RP SEQUENCE OF 1-11 FROM N.A.
RA Garibay-Tupas J.;
"Characterization of the human H1 relaxin 5'-flanking region."
Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
-!- FUNCTION: Relaxin is an ovarian hormone that acts with estrogen to
produce dilatation of the birth canal in many mammals. May be
involved in remodeling of connective tissues during pregnancy,
promoting growth of pubic ligaments and ripening of the cervix.
-!- SUBUNIT: Heterodimer of a B chain and an A chain linked by two
disulfide bonds.
-!- SUBCELLULAR LOCATION: Secreted.
-!- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
Name=1;
IsoId=PC4808-1; Sequence=Displayed;
Name=2;
IsoId=PC4808-2; Sequence=VSP_002709; VSP_002710;
-!- TISSUE SPECIFICITY: Prostate. Not expressed in placenta, decidua
or ovary.
-!- SIMILARITY: Belongs to the insulin family.
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EMBL; X00949; CAA25461.1; -
EMBL; V00578; CAA23839.1; -
EMBL; V00577; CAA23838.1; -
EMBL; AF104934; AAD21967.1; -
EMBL; A06926; CAA00603.1; -

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EMBL; A06846; CAA00599.1; -
EMBL; A07364; CAA00658.1; -
EMBL; A17329; CAA01325.1; -
EMBL; AL135786; CAC04179.1; -
EMBL; BC005956; AA005956.1; -
EMBL; S83200; AAD14429.1; -
PIR; B05092; A44559.
HSP; P04090; 6RLX.
Genew; HGNC:10026; RLN1.
MIM; 179730; -
GO; GO:0005180; F:peptide hormone; TAS.
InterPro; IPR004825; Ins/IGF/relax.
Pfam; PF00049; Insulin; 1.
SMART; SM00078; IIGF; 1.
PROSITE; PS00262; INSULIN; 1.
Insulin family; Hormone; Multigene family; Signal;
Alternative splicing; Polymorphism.
SIGNAL 1 22
CHAIN 23 53
PROPEP 56 158
CHAIN 163 185
DISULFID 35 172
DISULFID 47 185
DISULFID 171 176
VARSPLIC 71 117
VARSPLIC 118 185
VARIANT 28 28
K -> M (in dbSNP:618066).
/FTID=VAR_011962.
SEQUENCE 185 AA; 21145 MW; B318628ABFE7142 CRC64;
Query Match 37.4%; Score 46; DB 1; Length 185;
Best Local Similarity 43.8%; Pred. No. 5.3;
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
|||||
4 RCCLIPACRNNHKKFC 19
170 KCCLIGCKYRSIAKVC 185
MULT 11
11 CHICK
WFD1 CHICK STANDARD; PRT; 222 AA.
O8J33.
10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
WAP four-disulfide core domain protein 1 precursor (ps20 protein).
WFD01 OR PS20.
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
Gallus.
NCBI_TaxID=9031;
[1]
SEQUENCE FROM N.A.
Lopez-Viado C., Galletto R., Piedra E., Ros M., Rodriguez-Rey J.C.;
"cp20 is differentially expressed in chicken limb buds.";
Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
-!- FUNCTION: Has growth inhibitory activity (By similarity).
-!- SUBCELLULAR LOCATION: Secreted (potential).
-!- SIMILARITY: Contains 1 WAP-type domain.
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-----
EMBL; AJ438290; CAD27352.1; -
DR InterPro; IPR008197; WAP.
DR Pfam; PF00095; wap; 1.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4 DISULFIDE CORE; 1.
KW Serine protease inhibitor; Signal.
FT SIGNAL 1 32
FT CHAIN 33 222
FT DOMAIN 64 109
FT DOMAIN 69 72
FT DISULFID 68 98
FT DISULFID 80 102
FT DISULFID 85 97
FT DISULFID 91 106
FT DISULFID 91 106
SQ SEQUENCE 222 AA; 25235 MW; CD8B00BD1CED5BEB CRC64;
Query Match 37.0%; Score 45.5; DB 1; Length 222;
Best Local Similarity 36.1%; Pred. No. 7.5;
Matches 8; Conservative 3; Mismatches 5; Indels 5; Gaps 1;
QY 4 RCCLIPACR-----RNHKKFC 19
DB 78 RCEVPSCRSDSECRHKCC 98
RESULT 12
ID IBBI_COILA STANDARD; PRT; 64 AA.
AC P07679;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Bowman-Birk type trypsin inhibitor TII.
OS Coix lachryma-jobi (Jobs' tears).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACAD clade; Panicoideae; Andropogoneae; Coix.
OX NCBI_TaxID=4505;
RN [1]
RP
RP SEQUENCE.
RX MEDLINE=89152203; PubMed=3162215;
RA Ary M.B., Shewry P.R., Richardson M.;
RT "The amino acid sequence of a cereal Bowman-Birk type trypsin
RT inhibitor from seeds of Jobs' tears (Coix lachryma-jobi L.)";
RL FEBS Lett. 229:111-118(1988).
CC -!- SIMILARITY: Belongs to the Bowman-Birk serine protease inhibitor
CC family.
CC PIR; S00349; TIOAB.
CC HSSP; P56679; IPBI.
DR InterPro; IPR000877; Bowman-Birk_leg.
DR Pfam; PF00228; Bowman-Birk_leg; 2.
DR ProDom; PD002168; Bowman-Birk_leg; 1.
DR SMART; SM00269; BOWB; 1.
DR PROSITE; PS00281; BOWMAN_BIRK; 1.
KW Serine protease inhibitor.
FT ACT SITE 17 18
FT DISULFID 9 61
FT DISULFID 10 25
FT DISULFID 15 23
FT DISULFID 32 39
FT DISULFID 36 49
SQ SEQUENCE 64 AA; 7270 MW; 2ED0EEFF063E891 CRC64;
Query Match 36.6%; Score 45; DB 1; Length 64;
Best Local Similarity 41.2%; Pred. No. 2.7;
Matches 7; Conservative 1; Mismatches 9; Indels 0; Gaps 0;
QY 3 WRCLIPACRNNHKKFC 19
DB 7 WECCDIAMCTRSIPIC 23
```

SULT 13

11\_ CXAI CONTE STANDARD; PRT; 69 AA.  
 Q9XZK6;  
 16-OCT-2001 (Rel. 40, Last sequence update)  
 16-OCT-2001 (Rel. 40, Last sequence update)  
 28-FEB-2003 (Rel. 41, Last annotation update)  
 Alpha-type conotoxin Tx1 precursor.  
 Conus textile (Cloth-of-gold cone).  
 Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;  
 Apogastropoda; Caenogastropoda; Sorbecconcha; Hypogastropoda;  
 Neogastropoda; Conoidea; Conidae; Conus.  
 NCBI\_TaxID=6494;  
 [1]  
 SEQUENCE FROM N.A.  
 TISSUE=Venom duct;  
 MEDLINE=20037955; PubMed=10573284;  
 Lu B.-S., Yu F., Zhao D., Huang P.-T., Huang C.-F.;  
 "Conopeptides from Conus striatus and Conus textile by cDNA  
 cloning.";  
 Peptides 20:1139-1144(1999).  
 -!- FUNCTION: Alpha-conotoxins act on postsynaptic membranes, they  
 bind to the nicotinic acetylcholine receptors (nAChR) and thus  
 inhibit them (by similarity).  
 -!- SUBCELLULAR LOCATION: Secreted.  
 -!- TISSUE SPECIFICITY: Expressed by the venom duct.  
 -!- SIMILARITY: Belongs to the conotoxin A-superfamily. Alpha-type  
 family.

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EMBL; AF146352; AAD31912.1;  
 Postsynaptic neurotoxin; Neurotoxin; Toxin;  
 Acetylcholine receptor inhibitor; Signal; Amidation.  
 SIGNAL 1 21  
 POTENTIAL.  
 PROPEP 22 49 BY SIMILARITY.  
 PEPTIDE 50 66 ALPHA-TYPE CONOTOXIN TX1.  
 DISULFID 51 57 BY SIMILARITY.  
 DISULFID 52 65 BY SIMILARITY.  
 MOD RES 66 66 AMIDATION (G-67 PROVIDE AMIDE GROUP).  
 SEQUENCE 69 AA; 7442 MW; E36ECE90BF1B56B0 CRC64;  
 Query Match 36.6%; Score 45; DB 1; Length 69;  
 Best Local Similarity 40.0%; Pred. No. 2.9;  
 Matches 6; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

5 CCLIPACRRNHKFC 19  
 ||| : : : : :  
 51 CCSDPRCNSSHPCLC 65

SULT 14

31\_ METJA STANDARD; PRT; 519 AA.  
 Q59025;  
 30-MAY-2000 (Rel. 39, Created)  
 30-MAY-2000 (Rel. 39, Last sequence update)  
 16-OCT-2001 (Rel. 40, Last annotation update)  
 Hypothetical protein MJ1631.  
 Methanococcus jannaschii.  
 Archaea; Euryarchaeota; Methanococci; Methanococcales;  
 Methanocaldococcaceae; Methanocaldococcus.  
 NCBI\_TaxID=2190;  
 [1]  
 SEQUENCE FROM N.A.  
 STRAIN=JAL-1 / DSM 2661 / ATCC 43067;

RX MEDLINE=96337999; PubMed=8688087;  
 RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,  
 RA Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,  
 RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,  
 RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,  
 RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,  
 RA Uitterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,  
 RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,  
 RA Klank H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;  
 "Complete genome sequence of the methanogenic archaeon, Methanococcus  
 jannaschii.";  
 Science 273:1058-1073(1996).  
 RL Science 273:1058-1073(1996).  
 CC -!- SIMILARITY: Belongs to the glycogen phosphorylase family.  
 CC  
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CC EMBL; U67603; AAB99652.1;  
 DR PIR; E64503; E64503.  
 DR TIGR; MJ1631.  
 DR InterPro; IPR000811; Glyco trans 35.  
 DR PROSITE; PS0102; PHOSPHORYLASE; FALSE\_NEG.  
 DR Hypothetical protein; Complete proteome.  
 KW SEQUENCE 519 AA; 60469 MW; D2C9D64C7C0D2093 CRC64;

Query Match 36.6%; Score 45; DB 1; Length 519;  
 Best Local Similarity 32.0%; Pred. No. 20;  
 Matches 8; Conservative 4; Mismatches 7; Indels 6; Gaps 1;

QY 1 FNRCCUIPACRR-----NHKFC 19  
 ||| : : : : :  
 DB 231 FNTVTCALRVCKRANAVSKKKEVC 255

RESULT 15

GRN\_HUMAN STANDARD; PRT; 593 AA.  
 ID GRN\_HUMAN STANDARD; P23782; P23783; P23784; Q95WE7;  
 AC P28799; P23781; P23782; P23783; P23784; Q95WE7;  
 DT 01-NOV-1991 (Rel. 20, Created)  
 DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Granulins precursor (Acrogranin) (Proepithelin) (PEPI) [Contains:  
 DE Paragranulin; Granulin 1 (Granulin G); Granulin 2 (Granulin F);  
 DE Granulin 3 (Granulin B); Granulin 4 (Granulin A); Granulin 5 (Granulin  
 DE C); Granulin 6 (Granulin D); Granulin 7 (Granulin E)].  
 GN GRN.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
 RC TISSUE=Bone marrow;  
 RX MEDLINE=92179253; PubMed=1542665;  
 RA Bhandari V., Palfrey R.G.E., Bateman A.;  
 RT "Isolation and sequence of the granulin precursor cDNA from human  
 RT bone marrow reveals tandem cysteine-rich granulin domains.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 89:1715-1719(1992).  
 RN [2]  
 RP REVISIONS, SEQUENCE FROM N.A.  
 RX MEDLINE=93038704; PubMed=1417868;  
 RA Bhandari V., Bateman A.;  
 RT "Structure and chromosomal location of the human granulin gene.";  
 RL Biochem. Biophys. Res. Commun. 188:57-63(1992).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Kidney;  
 RX MEDLINE=92317004; PubMed=1618805;

Plowman G.D., Green I.M., Neubauer M.G., Buckley S.D., McDonald V.L.,  
 Todaro G.J., Shoyab M.;  
 "The epithelin precursor encodes two proteins with opposing activities  
 on epithelial cell growth";  
 J Biol. Chem. 267:13073-13078 (1992).

[4]  
 SEQUENCE FROM N.A.  
 TISSUE=Brain;  
 Yu W., Gibbs R.A.;

Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.  
 [5]  
 SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).  
 TISSUE=Cervix, and Lung;

MEDLINE=22388257; PubMed=12477932;  
 Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,  
 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,  
 Raha S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 Fahey J., Helton E., Kettman M., Maman A., Rodriguez S., Sanchez A.,  
 Whiting M., Maman A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 "Generation and initial analysis of more than 15,000 full-length  
 human and mouse cDNA sequences";  
 Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903 (2002).

[6]  
 SEQUENCE OF 206-233; 281-336; 364-396 AND 442-447.  
 TISSUE=Leukocyte;

MEDLINE=91097544; PubMed=2268320;  
 Bateman A., Belcourt D.R., Bennett H.P., Lazure C., Solomon S.;  
 "Granulins, a novel class of peptide from leukocytes";  
 Biochem. Biophys. Res. Commun. 173:1161-1168 (1990).

-!- FUNCTION: Granulins have possible cytokine-like activity. They may  
 play a role in inflammation, wound repair, and tissue remodeling.  
 -!- FUNCTION: Granulin A promotes proliferation of the epithelial cell  
 line A431 in culture while granulin B acts as an antagonist to  
 granulin A, inhibiting the growth.

-!- SUBCELLULAR LOCATION: Secreted.

-!- ALTERNATIVE PRODUCTS:

Event=Alternative splicing; Named isoforms=2;

Name=1;

Isoid=P28799-1; Sequence=Displayed;

Name=2;

Isoid=P28799-2; Sequence=VSP\_001837;

Note=No experimental confirmation available;

-!- TISSUE SPECIFICITY: In myelogenous leukemic cell lines of

promonocytic, promyelocytic, and proerythroid lineage, in

fibroblasts, and very strongly in epithelial cell lines. Present

in inflammatory cells and bone marrow. Highest levels in kidney.

-!- PTM: Granulins are disulfide bridged.

-!- SIMILARITY: Belongs to the granulin family.

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EMBL; M75161; AA58617.1; ALT\_SEQ.

EMBL; X62320; CAA44196.1; -.

EMBL; AF055008; AAC09359.1; -.

EMBL; BC000324; AAH00324.1; -.

DR EMBL; BC010577; AAH10577.1; -.  
 DR PIR; JCI284; GYHU.  
 DR PDB; 1G36; 01-NOV-00.  
 DR GENE; HGNC:4601; GRN.  
 DR MIM; 138945; -.  
 DR GO; GO:0008083; F: growth factor activity; TAS.  
 DR InterPro; IPR000118; Granulin.  
 DR Pfam; PF00396; granulin; 7.  
 DR SMART; SM00277; GRAN; 7.  
 DR PROSITE; PS00799; GRANULINS; 7.  
 KW Cytokine; Repeat; Glycoprotein; Signal; Alternative splicing;  
 KW Polymorphism; 3D-structure.  
 FT SIGNAL 1 17 POTENTIAL.  
 FT CHAIN 18 593 ACROGRANIN.  
 FT PEPTIDE 18 747 PARAGRANULIN.  
 FT PEPTIDE 758 7113 GRANULIN 1.  
 FT PEPTIDE 7123 7179 GRANULIN 2.  
 FT PEPTIDE 205 261 GRANULIN 3.  
 FT PEPTIDE 281 336 GRANULIN 4.  
 FT PEPTIDE 364 7417 GRANULIN 5.  
 FT PEPTIDE 7518 7573 GRANULIN 6.  
 FT PEPTIDE 7518 7573 GRANULIN 7.  
 FT CARBOHYD 118 118 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 236 236 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 265 265 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 368 368 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 530 530 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT VARSPLIC 377 531 Missing (in isoform 2).  
 FT VARIANT 454 454 /FTIG=VSP\_001837.  
 FT VARIANT 454 454 G -> Q.  
 FT VARIANT 515 515 /FTIG=VAR\_003445.  
 FT VARIANT 515 515 G -> A (in dbSNP:25647).  
 FT CONFLICT 219 219 /FTIG=VAR\_014830.  
 FT CONFLICT 386 386 S -> H (IN REF. 6).  
 FT CONFLICT 593 593 W -> H (IN REF. 6).  
 SQ SEQUENCE 593 AA; 63473 MW; 4E402BDB16DE2819 CRC64;  
 Query Match 36.6%; Score 45; DB 1; Length 593;  
 Best Local Similarity 42.1%; Pred. No. 23;  
 Matches 8; Conservative 2; Mismatches 7; Indels 2; Gaps 1;  
 Qy 3 WRCLIP--ACRRNHKKFC 19  
 Db 386 WGCCPIPEAVCCSDHQHCC 404  
 RESULT 16  
 HSPI\_BOVIN  
 ID HSPI\_BOVIN STANDARD; PRT; 50 AA.  
 AC P02318;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 13-AUG-1987 (Rel. 05, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Sperm protamine P1 (Cysteine-rich protamine).  
 GN PRM1 OR PRM-1.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 CX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=87161234; PubMed=3829989;  
 RA Krawetz S.A., Connor W., Dixon G.H.;  
 RT "Cloning of bovine P1 protamine cDNA and the evolution of vertebrate  
 P1 protamines";  
 RL DNA 6:47-57 (1987).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=88087109; PubMed=3335501;  
 RA Krawetz S.A., Connor W., Dixon G.H.;  
 RT "Bovine protamine genes contain a single intron. The structures of  
 the two alleles.";

J. Biol. Chem. 263:321-326 (1988).

[3]  
SEQUENCE FROM N.A.  
MEDLINE=87184911; PubMed=2436637;  
Lee C.-H., Mansouri A., Hecht W., Hecht N.B., Engel W.;  
"Nucleotide sequence of a bovine protamine cDNA.";  
Biol. Chem. Hoppe-Seyler 368:131-135 (1987).  
[4]  
SEQUENCE.  
MEDLINE=86269988; PubMed=37030390;  
Mazrimas J.A., Corzett M., Campos C., Balhorn R.;  
"A corrected primary sequence for bull protamine.";  
Biochim. Biophys. Acta 872:11-15 (1986).  
[5]  
SEQUENCE.  
MEDLINE=73124384; PubMed=4675900;  
Coelingh J.P., Monfoort C.H., Rozijn T.H., Gevers Leuven J.A.,  
Schiphof R., Steyn-Parve E.P., Braunitzer G., Schrank B., Ruitus A.;  
"The complete amino acid sequence of the basic nuclear protein of  
bull spermatozoa.";  
Biochim. Biophys. Acta 285:1-14 (1972).  
[6]  
DISULFIDE BONDS.  
MEDLINE=91105078; PubMed=1988019;  
Balhorn R., Corzett M., Mazrimas J., Watkins B.;  
"Identification of bull protamine disulfides.";  
Biochemistry 30:175-181 (1991).  
-!- FUNCTION: Protamines substitute for histones in the chromatin of  
sperm during the haploid phase of spermatogenesis. They compact  
sperm DNA into a highly condensed, stable and inactive complex.  
-!- SUBUNIT: Cross-linked by interchain disulfide bonds around the  
DNA-helix.  
-!- SUBCELLULAR LOCATION: Nuclear.  
-!- TISSUE SPECIFICITY: Testis.  
-!- SIMILARITY: Belongs to the protamine P1 family.  
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EMBL; M14559; AAA30741.1; -;  
EMBL; M18396; AAA30735.1; -;  
EMBL; M18395; AAA30736.1; -;  
EMBL; M18625; AAA30742.1; -;  
PIR; A23911; HSBOS.  
InterPro: IPR000221; Protamine\_P1.  
Pfam: PF00260; protamine P1; 1.  
PROSITE: PS00048; PROTAMINE\_P1; 1.  
Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding;  
Testis; DNA condensation; Nuclear protein.  
INIT MET 0 0 INTERCHAIN (WITH C-22).  
DISULFID 5 5  
DISULFID 6 14  
DISULFID 22 22 INTERCHAIN (WITH C-5).  
DISULFID 38 38 INTERCHAIN (WITH C-38).  
DISULFID 39 47  
CONFLICT 29 29 F -> S (IN REF. 3).  
CONFLICT 39 41 MISSING (IN REF. 5).  
SEQUENCE 50 AA; 6627 MW; 932A69D98D30D2C7 CRC64;

Query Match 36.2%; Score 44.5; DB 1; Length 50;  
Best Local Similarity 40.0%; Pred. No. 2.6;  
Matches 8; Conservative 4; Mismatches 5; Indels 3; Gaps 1;  
3 WRCCLIIPA---CRNHKKFC 19  
:||||:||||:  
3 YRCCLTHSGRCRRRRRC 22

RESULT 17  
HSP1 SHEEP STANDARD; PRT; 50 AA.  
ID HSP1 SHEEP  
AC P04102;  
DT 01-NOV-1986 (Rel. 03, Created)  
DT 01-NOV-1986 (Rel. 03, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Sperm protamine P1 (Cysteine-rich protamine).  
GN PRM1 OR PRM-1.  
OS Ovis aries (Sheep), and  
OS Capra hircus (Goat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Caprinae; Ovis.  
OX NCBI\_TaxID=9940, 9925;  
RN [1]  
RP SEQUENCE.  
RC SPECIES=Sheep;  
RX MEDLINE=85003651; PubMed=6479168;  
RA Sautiere P., Belaiche D., Martinage A., Loir M.;  
RT "Primary structure of the ram (Ovis aries) protamine.";  
RL Eur. J. Biochem. 144:121-125 (1984).  
RN [2]  
RP SEQUENCE.  
RC SPECIES=C. hircus;  
RX MEDLINE=89078594; PubMed=3060372;  
RA Ammer H., Henschen A.;  
RT "Primary structure of rabbit sperm protamine, the first protamine of  
its type with an aberrant N-terminal.";  
RL FEBS Lett. 242:111-115 (1988).  
CC -!- FUNCTION: Protamines substitute for histones in the chromatin of  
sperm during the haploid phase of spermatogenesis. They compact  
sperm DNA into a highly condensed, stable and inactive complex.  
CC -!- SUBUNIT: Cross-linked by interchain disulfide bonds around the  
DNA-helix (By similarity).  
CC -!- SUBCELLULAR LOCATION: Nuclear.  
CC -!- TISSUE SPECIFICITY: Testis.  
CC -!- SIMILARITY: Belongs to the protamine P1 family.  
DR PIR; A02658; HSSH.  
DR InterPro; IPR000221; Protamine\_P1.  
DR Pfam; PF00260; protamine P1; 1.  
DR PROSITE; PS00048; PROTAMINE\_P1; 1.  
KW Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding;  
KW Testis; DNA condensation; Nuclear protein.  
FT DISULFID 5 5 INTERCHAIN (WITH C-22) (BY SIMILARITY).  
FT DISULFID 6 14 BY SIMILARITY.  
FT DISULFID 22 22 INTERCHAIN (WITH C-5) (BY SIMILARITY).  
FT DISULFID 38 38 INTERCHAIN (WITH C-38) (BY SIMILARITY).  
FT DISULFID 39 47 BY SIMILARITY.  
SQ SEQUENCE 50 AA; 6712 MW; 6B2A78D98D2242DA CRC64;  
Query Match 36.2%; Score 44.5; DB 1; Length 50;  
Best Local Similarity 40.0%; Pred. No. 2.6;  
Matches 8; Conservative 4; Mismatches 5; Indels 3; Gaps 1;  
QY 3 WRCCLIIPA---CRNHKKFC 19  
:||||:||||:  
Db 3 YRCCLTHSGRCRRRRRC 22  
RESULT 18  
ALDR MOUSE STANDARD; PRT; 315 AA.  
ID ALDR MOUSE  
AC P45376; O70130; Q99KC9;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Aldose reductase (EC 1.1.1.21) (AR) (Aldehyde reductase).  
GN AKR1B1 OR ALDR1 OR ALDR1.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI\_TaxID=10090;



[1] SEQUENCE FROM N.A.  
 STRAIN=C57BL/6; TISSUE=Kidney;  
 MEDLINE=95154325; PubMed=7851421;  
 Gui T., Tanimoto T., Kokai Y., Nishimura C.;  
 "Presence of a closely related subgroup in the aldo-ketoreductase  
 family of the mouse.";  
 Eur. J. Biochem. 227:448-453 (1995).

[2] SEQUENCE FROM N.A.  
 STRAIN=ICR X Swiss Webster; TISSUE=Liver;  
 Iwata T., Carper B.;  
 Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.

[3] SEQUENCE FROM N.A.  
 STRAIN=CD-1; TISSUE=Kidney;  
 Daoudal S., Berger M., Pailhoux E., Tournaire C., Veyssiere G.,  
 Jean C.;  
 Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.

[4] SEQUENCE FROM N.A.  
 STRAIN=129/Ola;  
 MEDLINE=98153248; PubMed=9485495;  
 McGowan M.H., Iwata T., Carper D.A.;  
 "Characterization of the mouse aldose reductase gene and promoter in a  
 lens epithelial cell line.";  
 Mol. Vision 4:2-2 (1998).

[5] SEQUENCE FROM N.A.  
 STRAIN=129/SVJ;  
 MEDLINE=99192817; PubMed=10092857;  
 Ho H.T.B., Jenkins N.A., Copeland N.G., Gilbert D.J., Winkles J.A.,  
 Louie H.W.Y., Lee F.K., Chung S.S.M., Chung S.K.;  
 "Comparisons of genomic structures and chromosomal locations of the  
 mouse aldose reductase and aldose reductase-like genes.";  
 Eur. J. Biochem. 259:726-730 (1999).

[6] SEQUENCE FROM N.A.  
 STRAIN=BALB/c;  
 MEDLINE=99160426; PubMed=10049784;  
 Li H., Nobukuni Y., Gui T., Yabe-Nishimura C.;  
 "Characterization of genomic regions directing the cell-specific  
 expression of the mouse aldose reductase gene.";  
 Biochem. Biophys. Res. Commun. 255:759-764 (1999).

[7] SEQUENCE FROM N.A.  
 TISSUE=Breast;  
 MEDLINE=92386257; PubMed=12477932;  
 Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 Stapleton M., Soares M.B., Donaldson M.F., Casavant T.L., Scheetz T.E.,  
 Brownstein M.J., Udén T.B., Toshyiki S., Carninci P., Prange C.,  
 Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 Whiting M., Madan A., Young A.C., Shcherenko Y., Bouffard G.G.,  
 Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 "Generation and initial analysis of more than 15,000 full-length  
 human and mouse cDNA sequences";  
 Proc. Natl. Acad. Sci. U.S.A. 99:15899-15903 (2002).

-!- FUNCTION: Catalyzes the NADPH-dependent reduction of a wide  
 variety of carbonyl-containing compounds to their corresponding  
 alcohols with a broad range of catalytic efficiencies.

-!- CATALYTIC ACTIVITY: Alditol + NAD(P)(+) = aldose + NAD(P)H.

-!- SUBUNIT: Monomer.

CC -!- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -!- TISSUE SPECIFICITY: Abundant in the testis, skeletal muscle and  
 CC kidney.  
 CC -!- SIMILARITY: Belongs to the aldo/keto reductase family.  
 CC  
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 CC  
 CC EMBL; D32250; BAA06980.1; -  
 CC EMBL; L39795; AAA62176.1; -  
 CC EMBL; U29152; AAA69958.1; -  
 CC EMBL; U89150; AAC13358.1; -  
 CC EMBL; U89140; AAC13358.1; JOINED.  
 CC EMBL; U89142; AAC13358.1; JOINED.  
 CC EMBL; U89143; AAC13358.1; JOINED.  
 CC EMBL; U89144; AAC13358.1; JOINED.  
 CC EMBL; U89145; AAC13358.1; JOINED.  
 CC EMBL; U89146; AAC13358.1; JOINED.  
 CC EMBL; U89147; AAC13358.1; JOINED.  
 CC EMBL; U89148; AAC13358.1; JOINED.  
 CC EMBL; U89149; AAC13358.1; JOINED.  
 CC EMBL; U93231; AAD32300.1; -  
 CC EMBL; U93230; AAD32300.1; JOINED.  
 CC EMBL; AB016665; BAA76413.1; -  
 CC EMBL; AB016662; BAA76413.1; JOINED.  
 CC EMBL; AB016663; BAA76413.1; JOINED.  
 CC EMBL; AB016664; BAA76413.1; JOINED.  
 CC EMBL; BC004725; BAA04725.1; -  
 CC EMBL; BC021655; BAA21655.1; -  
 CC F1R; I49484; I49484.  
 CC HSSP; F15121; 2ACQ.  
 CC PMWA-2DPAGE; P45376; MOUSE.  
 CC MGD; MGI:1353494; Akribi.  
 CC InterPro; IPR001395; Aldo/ket\_red.  
 CC Pfam; PF00248; aldo\_ket\_red; 1.  
 CC PRINTS; P00089; ALDOKETREDTASE.  
 CC ProDom; PD000288; Aldo/ket\_red; 1.  
 CC PROSITE; PS00062; ALDOKETO\_REDUCTASE\_2; 1.  
 CC PROSITE; PS00063; ALDOKETO\_REDUCTASE\_3; 1.  
 CC PROSITE; PS00798; ALDOKETO\_REDUCTASE\_1; 1.  
 CC Oxidoreductase; NADP; acetylation; Multigene family.  
 KW INIT\_MET 0 0 BY SIMILARITY.  
 FT NP\_BIND 9 18 NADP (POTENTIAL).  
 FT ACT\_SITE 48 48 HYDROGEN-BOND DONOR (BY SIMILARITY).  
 FT MOD\_RES 1 1 ACETYLATION (BY SIMILARITY).  
 FT CONFLICT 45 45 A -> S (IN REF. 1).  
 FT CONFLICT 220 220 A -> G (IN REF. 4).  
 FT CONFLICT 280 280 V -> L (IN REF. 7).  
 SQ SEQUENCE 315 AA; 35601 MW; 607E604FF432580E CRC64;  
 Query Match 36.2%; Score 44.5; DB 1; Length 315;  
 Best Local Similarity 41.2%; Pred. No. 15;  
 Matches 7; Conservative 4; Mismatches 5; Indels 1; Gaps 1;  
 QY 2 NWRCCLIIPACRNHKKF 18  
 DB 294 NWRVCAIMSCAK-HXDY 309  
 RESULT 19  
 ALDR RAT  
 ID ALDR RAT STANDARD; PRT; 315 AA.  
 AC P07943;  
 DT 01-NOV-1998 (Rel. 08, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Aldose reductase (EC 1.1.1.21) (AR) (Aldehyde reductase).





```
SEQUENCE 16 AA; 1716 MW; 282AEF190166CAF9 CRC64;
Query Match 35.8%; Score 44; DB 1; Length 16;
Best Local Similarity 40.0%; Pred. No. 1;
Matches 6; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

5 CCLIPACRRNHKKFC 19
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2 CCNPNVCHLEHSLC 16

SULT 23
31 SCHPO
RCCL SCHPO STANDARD; PRT; 271 AA.
094448;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Probable CAAX prenyl protease 2 (EC 3.4.22.-) (Prenyl protein-specific
endoprotease 2) (PPSEP 2).
SPAC1687.02.
Schizosaccharomyces pombe (Pission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
Schizosaccharomycetes.
NCBI_TaxID=4896;
[1]
SEQUENCE FROM N.A.
STRAIN=972;
MEDLINE=21848401; PubMed=11859360;
Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
Collins M., Connor R., Cronin A., Davis P., Felwell T., Fraser A.,
Gentles S., Godle A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
Skilton J., Simmonds M., Squares R., Squares K., Stevens K.,
Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
Woodward J., Voiclaert G., Aert R., Robben J., Grymonprez B.,
Waltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
Borzym K., Langer I., Beck A., Leirach H., Reinhardt R., Pohl T.M.,
Eger P., Zimmermann W., Wedler H., Wamburt R., Purnelle B.,
Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Rhode G.,
Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
"the genome sequence of Schizosaccharomyces pombe";
Nature 415:871-880(2002).
-!- FUNCTION: Proteolytically removes the C-terminal three residues of
farnesylated proteins (By similarity).
-!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
reticulum (By similarity).
-!- SIMILARITY: Belongs to peptidase family U48.
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EMBL; AL035064; CAA22596.1; -
PIR; T37745; T37745.
MEROPS; U48.OPW; -
DR GenedB SPombe; SPAC1687.02; -
DR InterPro; IPR003675; Abi.
DR Pfam; PF02517; Abi.1
KW Hypothetical protein; Hydrolase; Transmembrane; Endoplasmic reticulum.
FT TRANSMEM 3 23
FT TRANSMEM 42 62 POTENTIAL.
FT TRANSMEM 174 194 POTENTIAL.
FT TRANSMEM 236 256 POTENTIAL.
SQ SEQUENCE 271 AA; 31024 MW; 7274E9BE25348BB CRC64;
Query Match 35.8%; Score 44; DB 1; Length 271;
Best Local Similarity 55.6%; Pred. No. 15;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 3 WRCLIPAC 11
|||
DB 130 FRCCIVPIC 138
|||
RESULT 24
ALD2 MOUSE
ID ALD2 MOUSE STANDARD; PRT; 315 AA.
AC P45377;
DC 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Aldose reductase-related protein 2 (EC 1.1.1.21) (AR) (Aldehyde
reductase) (Fibroblast growth factor regulated protein) (FR-1
protein).
DE protein.
GN AKR1B8 OR FGFRP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
[1]
RN RP
SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX MEDLINE=94179253; PubMed=7510692;
RA Donohue P.J., Alberts G.F., Hampton B.S., Winkles J.A.;
" A delayed-early gene activated by fibroblast growth factor-1 encodes
a protein related to aldose reductase.";
J. Biol. Chem. 269:8604-8609(1994).
[2]
RN RP
X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).
MEDLINE=96062495; PubMed=7578036;
RA Wilson D.K., Nakano T., Petrash M., Quirocho F.A.;
"1.7-A structure of FR-1, a fibroblast growth factor-induced member
of the aldo-keto reductase family, complexed with coenzyme and
inhibitor.";
Biochemistry 34:14323-14330(1995).
RL Biochemistry 34:14323-14330(1995).
CC -!- CATALYTIC ACTIVITY: Alditol + NAD(P)(+) = aldose + NAD(P)H.
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- INDUCTION: By FGF-1.
CC -!- SIMILARITY: Belongs to the aldo/keto reductase family.
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```

PROSITE; PS00063; ALDO-KETO REDUCTASE 3; 1.  
PROSITE; PS00798; ALDO-KETO REDUCTASE 1; 1.  
Oxidoreductase; NADP; Multigene family; 3D-structure.  
INIT MET 0 0  
BY SIMILARITY.  
ACT SITE 48 48  
HYDROGEN-BOND DONOR (BY SIMILARITY).  
STRAND 3 5  
TURN 7 8  
STRAND 11 13  
STRAND 15 15  
STRAND 17 18  
TURN 20 21  
HELIX 24 36  
TURN 37 38  
STRAND 41 43  
HELIX 46 48  
TURN 49 49  
HELIX 51 63  
TURN 64 65  
HELIX 69 71  
STRAND 73 78  
HELIX 80 82  
HELIX 85 99  
TURN 100 100  
STRAND 104 109  
STRAND 115 115  
STRAND 124 124  
TURN 126 127  
STRAND 130 130  
STRAND 132 132  
HELIX 137 149  
TURN 150 151  
STRAND 153 159  
HELIX 163 170  
TURN 171 171  
TURN 173 174  
STRAND 181 185  
STRAND 187 187  
TURN 188 189  
STRAND 190 190  
HELIX 193 201  
TURN 202 203  
STRAND 205 209  
TURN 211 212  
TURN 215 216  
TURN 218 219  
TURN 222 223  
TURN 227 229  
HELIX 231 239  
TURN 240 241  
HELIX 244 253  
TURN 254 256  
STRAND 258 259  
STRAND 262 262  
HELIX 266 273  
STRAND 282 289  
TURN 290 291  
HELIX 301 303  
TURN 304 305  
TURN 307 308  
TURN 311 312  
SEQUENCE 315 AA; 35989 MW; 8D9633994A3F5B7C CRC64;

Query Match 35.8%; Score 44; DB 1; Length 315;  
Best Local Similarity 75.0%; Pred. No. 17;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

2 NWRCLIP 9

294 NWRACLLP 301

SULT 25  
DH\_ANYME

ID P80594; STANDARD; PRT; 360 AA.  
AC  
DT 01-DEC-1992 (Rel. 24, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE NAD/mycothiol-dependent formaldehyde dehydrogenase (EC 1.2.1.66) (MD-FALDH)  
OS Amycolatopsis methanolica.  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Pseudonocardiaceae; Pseudonocardiaceae; Amycolatopsis.  
NCBI\_TaxID=1814;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=98004265; PubMed=9346279;  
RA Norin A., van Ophem P.W., Piersma S.R., Persson B., Duine J.A., Joernvall H.;  
RA "Mycothiol-dependent formaldehyde dehydrogenase, a prokaryotic medium-chain dehydrogenase/reductase, phylogenetically links different eukaryotic alcohol dehydrogenases -- primary structure, conformational modelling and functional correlations."; Eur. J. Biochem. 248:282-289(1997).  
RN [2]  
RP PRELIMINARY SEQUENCE OF 1-31.  
RX MEDLINE=92283278; PubMed=1597190;  
RA van Ophem P.W., van Beeumen J., Duine J.A.;  
RT "NAD-linked, factor-dependent formaldehyde dehydrogenase or trimeric, zinc-containing, long-chain alcohol dehydrogenase from Amycolatopsis methanolica."; Eur. J. Biochem. 206:511-518(1992).  
RN [3]  
RP CHARACTERIZATION.  
RX MEDLINE=97345657; PubMed=9202149;  
RA Misset-Smits M., van Ophem P.W., Sakuda S., Duine J.A.;  
RT "Mycothiol, 1-O-(2'-[N-acetyl-L-cysteinyllamido-2'-deoxy-alpha-D-glucopyranosyl)-D-myo-inositol, is the factor of NAD/factor-dependent formaldehyde dehydrogenase."; FEBS Lett. 409:221-222(1997).  
RL  
CC -!- CATALYTIC ACTIVITY: Formaldehyde + mycothiol + NAD(+) = S-formylmycothiol + NADH.  
CC -!- COFACTOR: Binds 2 zinc ions per subunit (By similarity).  
CC -!- SUBUNIT: Homotrimer.  
CC -!- SIMILARITY: Belongs to the zinc-containing alcohol dehydrogenase family.  
DR InterPro; IPR002328; ADH\_zinc.  
DR InterPro; IPR02085; Adh\_zn\_family.  
DR InterPro; IPR00205; NAD\_BS.  
DR Pfam; PF00107; ADH\_zinc\_N; 1.  
DR PROSITE; PS00059; ADH\_ZINC; 1.  
KW Oxidoreductase; Zinc; Metal-binding; NAD.  
FT ACT SITE 89 89 SUBSTRATE BINDING (PROBABLE).  
FT METAL 41 41 ZINC 1 (CATALYTIC (BY SIMILARITY)).  
FT METAL 62 62 ZINC 1 (CATALYTIC (BY SIMILARITY)).  
FT METAL 92 92 ZINC 2 (BY SIMILARITY).  
FT METAL 95 95 ZINC 2 (BY SIMILARITY).  
FT METAL 98 98 ZINC 2 (BY SIMILARITY).  
FT METAL 106 106 ZINC 2 (BY SIMILARITY).  
FT METAL 161 161 ZINC 1 (CATALYTIC (BY SIMILARITY)).  
SQ SEQUENCE 360 AA; 37757 MW; 48BED1F70EAB2C57 CRC64;

Query Match 35.8%; Score 44; DB 1; Length 360;  
Best Local Similarity 40.0%; Pred. No. 20;  
Matches 8; Conservative 3; Mismatches 7; Indels 2; Gaps 1;

QY 2 NWR--CCLIPACRENHKKFC 19

DB 87 NWRVCGGCRACKGRQPYC 106

RESULT 26

SECS HUMAN

ID SECS HUMAN STANDARD; PRT; 924 AA.

AC Q96KFL; Q96KNG; Q9NUZ8; Q9UJW7;

DT 28-FEB-2003 (Rel. 41, Created)

28-FEB-2003 (Rel. 41, Last sequence update)  
15-MAR-2004 (Rel. 43, Last annotation update)  
Exocyst complex component Sec5.

SEC5 OR SEC5L1

Homo sapiens (Human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
NCBI\_TaxID=9606;

[1] SEQUENCE FROM N.A., TISSUE SPECIFICITY, AND INTERACTION WITH GNEFR.  
MEDLINE=22347268; PubMed=12459492;

Sjoelinder M., Uhlmann J., Ponstingl H.;

"DELGF", a homologue of the Ran guanine nucleotide exchange factor  
RANGF, binds to the exocyst component Sec5 and modulates secretion."  
FEBS Lett. 532:211-215 (2002).

[2] SEQUENCE OF 1-793 FROM N.A.

Whitaker H.;

Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.

[3] SEQUENCE OF 119-924 FROM N.A.

TISSUE=Breast;

MEDLINE=22388257; PubMed=12477932;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,  
Diatchenko L., Marusina K., Farmer A.A., Rubin G.W., Hong L.,  
Sapleotn M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,  
Brownstein M.J., Uslin T.B., Toshiyuki S., Carninci P., Prange C.,  
Raha S.S., Loughran N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
Bosak S.A., Mcwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Rulyk S.W.,  
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,  
Fanev J., Heiton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
Butterfield Y.S.N., Krzywicki M.I., Skalska U., Smailus D.E.,  
Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;  
"Generation and initial analysis of more than 15,000 full-length  
human and mouse cDNA sequences.";  
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

[4] SEQUENCE OF 143-924 FROM N.A.

TISSUE=Placenta;

Isoqai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,  
Nishikawa T., Nagai K., Sugano S., Aotsuka S., Yoshikawa Y.,  
Matsunawa H., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A.,  
Nakamura Y., Negahari K., Masuho Y., Sasaki N.;

"NEDO human cDNA sequencing project.";

Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.

-!- FUNCTION: Component of the exocyst complex involved in the docking

of exocystic vesicles with fusions site on the plasma membrane.

-!- SUBUNIT: The exocyst complex is composed of SEC3, SEC5, SEC6,

SEC8, SEC10, SEC15, EXO70 and EXO84. Interacts with RALA and

GNEFR/DELGF. Interaction with GNEFR occurs only in the presence

of magnesium or manganese and is stimulated by dCTP or GTP.

-!- TISSUE SPECIFICITY: Widely expressed with highest levels in brain

and placenta.

-!- DOMAIN: Interacts with RALA through the TIG domain (By

similarity).

-!- SIMILARITY: Belongs to the SEC5 family.

-!- SIMILARITY: Contains 1 TIG domain.

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send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
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DR EMBL; AJ411403; CAC92092.1; -;  
DR EMBL; AL031770; -; NOT ANNOTATED CDS.  
DR EMBL; BC016918; AAH16918.1; ALT\_INIT.  
DR EMBL; AK001888; BAA91963.1; ALT\_INIT.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR002909; IFT\_TIG.  
DR Pfam; PF01833; TIG; 1.  
DR Exocytosis; Transport; Protein transport; Coiled coil.  
FT DOMAIN 8 93  
FT DOMAIN 240 260 COILED COIL (POTENTIAL).  
FT CONFLICT 522 522 L -> H (IN REF. 4).  
SQ SEQUENCE 924 AA; 104066 MW; 2234E463D8B076F CRC64;  
Query Match 35.8%; Score 44; DB 1; Length 924;  
Best Local Similarity 47.1%; Pred. NO. 49;  
Matches 8; Conservative 3; Mismatches 6; Indels 0; Gaps 0;  
QY 1 FNWRCCLIPACRRNHKK 17  
DB 784 FDKDKCLPPTGVRNLYK 800  
RESULT 27  
ALDR PIG STANDARD; PRT; 315 AA.  
AC P80276;  
DT 01-FEB-1994 (Rel. 28, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Aldose reductase (EC 1.1.1.21) (AR) (Aldohyde reductase).  
GN AKR1B1 OR ALR2.  
OC Eukarya; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
OC NCBI\_TaxID=9823;  
RN [1]  
RP SEQUENCE, MASS SPECTROMETRY, AND DISULFIDE BOND.  
RC TISSUE=Lens;  
RX MEDLINE=94109388; PubMed=8281941;  
RA Jaquinod M., Potier N., Klarskov K., Reyman J.-M., Sorokine O.,  
Kieffer S., Barth P., Andrianomanga V., Biellmann J.-F.,  
van Dorsselaer A.,  
RT "Sequence of pig lens aldose reductase and electrospray mass  
spectrometry of non-covalent and covalent complexes.";  
Eur. J. Biochem. 218:893-903 (1993).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=93263021; PubMed=8493902;  
RA Kubieski T.J., Green N.C., Flynn T.G.;

-!- CATALYTIC ACTIVITY: Alditol + NAD(P)(+) = aldose + NAD(P)H.  
 -!- SUBUNIT: Monomer.  
 -!- SUBCELLULAR LOCATION: Cytoplasmic.  
 -!- MASS SPECTROMETRY: MW=35778; MW ERR=3; METHOD=Electrospray.  
 -!- SIMILARITY: Belongs to the aldo/keto reductase family.

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EMBL; L14950; AAC30989.1; -

EMBL; U46085; AAC48515.1; -

FIR; AS9021; AS9021.

PDB; 1DLA; 30-APR-94.

PDB; 1AH0; 15-APR-98.

PDB; 1AH3; 15-APR-98.

PDB; 1AH4; 15-APR-98.

PDB; 1EKO; 10-MAY-00.

InterPro; IPR001395; Aldo/ket red.

Prims; PR00248; aldo\_ket\_red; 1.

PRINTS; PR00069; ALDKETDASE.

ProDom; PD000288; Aldo/ket red; 1.

PROSITE; PS00062; ALDO/KETO REDUCTASE 2; 1.

PROSITE; PS00063; ALDO/KETO REDUCTASE 3; 1.

PROSITE; PS00798; ALDO/KETO REDUCTASE 1; 1.

Oxidoreductase; NADP; Acetylation; 3D-structure.

INIT MET 0

NP\_BIND 0

ACT\_SITE 9 18 NADP (POTENTIAL).

MOD\_RES 48 48 HYDROGEN-BOND DONOR (BY SIMILARITY).

DISULFID 298 303 ACETYLATION.

CONFLICT 98 98 D -> N (IN REF. 2).

STRAND 3 5

TURN 7 8

STRAND 11 13

STRAND 15 15

STRAND 17 18

TURN 20 21

HELIX 24 37

TURN 38 38

STRAND 41 43

HELIX 46 48

HELIX 51 63

TURN 64 65

HELIX 69 71

STRAND 73 78

HELIX 80 82

HELIX 85 87

HELIX 88 99

TURN 100 100

STRAND 104 104

STRAND 106 109

STRAND 115 115

STRAND 124 124

TURN 126 127

STRAND 130 130

STRAND 132 132

HELIX 137 150

TURN 151 151

STRAND 153 153

STRAND 156 159

HELIX 163 170

TURN 171 171

TURN 173 174

STRAND 181 185

STRAND 187 187

TURN 188 189

STRAND 190 190

HELIX 193 202

PT TURN 203 203  
 FT STRAND 205 209  
 FT TURN 211 212  
 FT TURN 215 216  
 FT TURN 218 219  
 FT TURN 222 223  
 FT TURN 227 229  
 FT HELIX 231 240  
 FT TURN 241 241  
 FT HELIX 244 254  
 FT TURN 255 256  
 FT STRAND 258 259  
 FT STRAND 262 262  
 FT HELIX 266 271  
 FT TURN 272 277  
 FT HELIX 282 289  
 FT TURN 290 291  
 FT HELIX 301 303  
 FT TURN 304 305  
 FT TURN 307 308  
 FT HELIX 310 312  
 SQ SEQUENCE 315 AA; 35737 MW; F3E18F814E225C92 CRC64;

Query Match 35.4%; Score 43.5; DB 1; Length 315;  
 Best Local Similarity 41.2%; Pred.No.21;  
 Matches 7; Conservative 4; Mismatches 5; Indels 1; Gaps 1;

QY 2 NWRCLIPACRRNHKXF 18

DB 294 NWRVCLMSC-ASHKDY 309

RESULT 28

ALDR RABIT

ID ALDR RABIT STANDARD; PRT; 315 AA.

AC P15122;

DT 01-APR-1990 (Rel. 14, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Aldose reductase (EC 1.1.1.21) (AR) (Aldehyde reductase).

GN AKR1B1.

OS Oryctolagus cuniculus (Rabbit).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

OC NCBI\_TaxID=9986;

OX [1]

RP SEQUENCE FROM N.A.

RX TISSUE=Spleen;

RX MEDLINE=95024191; PubMed=7938022;

RA Ferraris J.D., Williams C.K., Martin B.M., Burg M.B., Garcia-Perez A.;

RA Cowley B.D. Jr., Handler J.S., Burg M.B.;

RT "Cloning, genomic organization, and osmotic response of the aldose

reductase gene.";

RL Proc. Natl. Acad. Sci. U.S.A. 91:10742-10746 (1994).

RN [2]

RP SEQUENCE OF 14-315 FROM N.A.

RP TISSUE=Kidney;

RX MEDLINE=89380313; PubMed=2506183;

RA Garcia-Perez A., Martin B., Murphy H.R., Uchida S., Murer H.,

RA Cowley B.D. Jr., Handler J.S., Burg M.B.;

RT "Molecular cloning of cDNA coding for kidney aldose reductase.

RT Regulation of specific mRNA accumulation by NaCl-mediated osmotic

stress.";

RL J. Biol. Chem. 264:16815-16821 (1989).

CC -!- FUNCTION: Catalyzes the NADPH-dependent reduction of a wide

variety of carbonyl-containing compounds to their corresponding

alcohols with a broad range of catalytic efficiencies.

CC -!- CATALYTIC ACTIVITY: Alditol + NAD(P)(+) = aldose + NAD(P)H.

CC -!- SUBUNIT: Monomer.

CC -!- SUBCELLULAR LOCATION: Cytoplasmic.

CC -!- SIMILARITY: Belongs to the aldo/keto reductase family.

CC -----

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EMBL; U13694; AAB60687.1; -.
EMBL; U13689; AAB60687.1; JOINED.
EMBL; U13690; AAB60687.1; JOINED.
EMBL; U13691; AAB60687.1; JOINED.
EMBL; U13692; AAB60687.1; JOINED.
EMBL; U13693; AAB60687.1; JOINED.
EMBL; M32818; AAA31150.1; -.
EMBL; U12316; AAA50833.1; -.
EMBL; J05048; AAA31157.1; -.
PIR; A34406; A34406.
HSSP; P15121; 2ACQ.
InterPro; IPR001395; Aldo/ket red.
Pfam; PF00248; aldo ket red; I.
PRINTS; PR00069; ALDXETREDTASE.
PRODOM; PD000288; Aldo/ket red; 1.
PROSITE; PS00062; ALDOKETO_REDUCTASE_2; 1.
PROSITE; PS00063; ALDOKETO_REDUCTASE_3; 1.
PROSITE; PS00798; ALDOKETO_REDUCTASE_1; 1.
Oxidoreductase; NADP; Acetylation.
INIT MET 0 0 BY SIMILARITY.
NP_BIND 9 18 NADP (POTENTIAL).
ACET SITE 48 48 HYDROGEN-BOND DONOR (BY SIMILARITY).
MOD RES 1 1 ACETYLATION (BY SIMILARITY).
SEQUENCE 315 AA; 56332 MW; 64D53E6AC0853FFB CR664;

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CC -----

CC EMBL; X96975; CAA65661.1; -.

CC HSSP; P06400; IGUX.

DR FLYBASE; FBgn0015799; Rbf.

DR GO; GO:0008285; P:negative regulation of cell proliferation; NAS.

DR InterPro; IPR006670; Cyclin.

DR InterPro; IPR002720; RB A.

DR InterPro; IPR002719; RB B.

DR Pfam; PF01858; RB A; 1.

DR Pfam; PF01857; RB B; 1.

DR SMART; SM00385; CYCLIN; 1.

KW Transcription regulation; DNA-binding; Nuclear protein; Cell cycle;

KW Phosphorylation.

FT DOMAIN 374 711 POCKET.

FT DOMAIN 374 566 DOMAIN A.

FT DOMAIN 576 711 DOMAIN B.

FT SEQUENCE 797 AA; 91910 MW; 5EA0C4638AA677303 CRC64;

Query Match 35.4%; Score 43.5; DB 1; Length 797;

Rest Local Similarity 61.5%; Pred. No. 50;

Matches 8; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

Qy 2 NWRCCL1-PACRR 13

Dd 68 HWMCCAIYTACRR 80

RESULT 30

JAG1\_HUMAN

ID JAG1\_HUMAN STANDARD; PRT; 1218 AA.

AC P78504; O14902; O15122; Q15816;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Jaggedl precursor (Jaggedl) [hul].

GN JAG1 OR JAGL1.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCBI\_TaxID=9606;

OR [1]

OR SEQUENCE FROM N.A.

OR MEDLINE=97422615; PubMed=9268641;

RA Oda T., Elkhahoun A.G., Meltzer P.S., Chandrasekharappa S.C.;

RT "Identification and cloning of the human homolog (JAG1) of the rat Jaggedl gene from the alagille syndrome critical region at 20p12.";

RL Genomics 43:376-379(1997).

RL [2]

RN SEQUENCE FROM N.A., AND VARIANT AGS CVS-184.

RP TISSUE=Bone marrow;

RC MEDLINE=97351506; PubMed=9207788;

RX Li L., Krantz I.D., Deng Y., Genin A., Banta A.B., Collins C.C., Qi M., Trask B.J., Kuo W.L., Cochran J., Costa T., Pierpont M.E.M., Rand E.B., Piccoli D.A., Hood L., Spinner N.B.;

RA "Alagille syndrome is caused by mutations in human Jaggedl, which encodes a ligand for Notch1.";

RT Nat. Genet. 16:243-251(1997).

RL [3]

RN SEQUENCE FROM N.A., AND FUNCTION.

RP MEDLINE=98122342; PubMed=9462510;

RX Li L., Milner L.A., Deng Y., Iwata M., Banta A.B., Graf L., Marcovina S., Friedman C., Trask B.J., Hood L., Torok-Storb B.;

PA "The human homolog of rat Jaggedl expressed by marrow stroma inhibits differentiation of 32d cells through interaction with Notch1.";

RT Immunity 8:43-55(1998).

RL [4]

RN SEQUENCE FROM N.A.

RP TISSUE=Cervical carcinoma;

RC MEDLINE=97351506; PubMed=9207788;

CC	EMBJ; X96975; CAA65661.1; -.		
DR	HSSP; P06400; 1GDX.		
DR	FlyBase; FBgn0015789; Rbf.		
DR	GO; GO:0008285; P:negative regulation of cell proliferation; NAS.		
DR	InterPro; IPR006670; Cyclin.		
DR	InterPro; IPR002720; RB A.		
DR	InterPro; IPR002719; RB B.		
DR	Pfam; PF01858; RB A; 1.		
DR	Pfam; PF01857; RB B; 1.		
DR	SMART; SM00385; CYCLIN; 1.		
KW	Transcription regulation; DNA-binding; Nuclear protein; Cell cycle; Phosphorylation.		
KW	POCKET.	711	
FT	DOMAIN	374	
FT	DOMAIN	374	566
FT	DOMAIN	576	711
FT	SEQUENCE	797 AA;	91910 MW; SEA0C4638A677303 CRC64;



- MEDLINE=99262417; PubMed=10329626;  
 Bash J., Zong W.-X., Barga S., Rivera A., Ballard D.W., Ron Y.,  
 Celinas C.  
 "Rel/NF-kappaB can trigger the Notch signaling pathway by inducing the  
 expression of Jagged1, a ligand for Notch receptors."  
 EMBO J. 18:2803-2811(1999).  
 [5]  
 SEQUENCE FROM N.A.  
 MEDLINE=99180765; PubMed=10079256;  
 Gray G.B., Mann R.S., Mitsiadis E.,  
 Banks A., Leiman J., Ward D., Ish-Horowitz D., Artavanis-Teakonas S.,  
 "Human ligands of the Notch receptor."  
 Am. J. Pathol. 154:785-794(1999).  
 [6]  
 SEQUENCE FROM N.A.  
 MEDLINE=21638749; PubMed=11780052;  
 Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,  
 Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,  
 Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,  
 Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,  
 Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,  
 Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,  
 Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,  
 Coulson A., Coville G.J., Deadman R., Dharm P.D., Dunn M.,  
 Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,  
 Graffham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,  
 Hammond S., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,  
 Huckle E., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,  
 Leharvelasho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,  
 Marsh V.L., Martin S.L., McConachie L.J., McLay K., McMurray A.A.,  
 Milne S.A., Mistry D., Moore M.J.P., Mullikin J.C., Nickerson T.,  
 Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,  
 Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramey H.,  
 Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkhen R., Sims S.,  
 Skuce C.D., Smith M.B., Soderlund C., Steward C.A., Sultston J.E.,  
 Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,  
 Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,  
 Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,  
 Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,  
 Rogers J.  
 "The DNA sequence and comparative analysis of human chromosome 20."  
 Nature 414:865-871(2001).  
 [7]  
 SEQUENCE OF 14-1227 FROM N.A.  
 TISSUE=Umbilical vein endothelial cells;  
 MEDLINE=97115768; PubMed=8955070;  
 Zimin A.B., Pepper M.S., McMahon G.A., Nguyen F., Montesano R.,  
 Maciag T.,  
 "an antisense oligonucleotide to the notch ligand jagged enhances  
 fibroblast growth factor-induced angiogenesis in vitro."  
 J. Biol. Chem. 271:32499-32502(1996).  
 [8]  
 DISEASE.  
 MEDLINE=97351505; PubMed=9207787;  
 Oda T., Elkahoul A.G., Pike B.L., Okajima K., Krantz I.D., Genin A.,  
 Piccoli D.A., Meitner P.S., Spinner N.B., Collins F.S.,  
 Chandrasekharappa S.C.;  
 "Mutations in the human Jagged1 gene are responsible for Alagille  
 syndrome."  
 Nat. Genet. 16:235-242(1997).  
 [9]  
 DEVELOPMENTAL STAGE.  
 MEDLINE=20436345; PubMed=10979356;  
 Jones E.A., Clement-Jones M., Wilson D.I.;  
 "JAGGED1 expression in human embryos: correlation with the Alagille  
 syndrome phenotype."  
 J. Med. Genet. 37:663-668(2000).  
 [10]  
 VARIANTS AGS CYS-184 AND HIS-184.  
 MEDLINE=98254456; PubMed=98585603;  
 Krantz I.D., Colliton R.P., Genin A., Rand E.B., Li L., Piccoli D.A.,  
 Spinner N.B.;  
 "Spectrum and frequency of jagged1 (JAG1) mutations in Alagille  
 syndrome patients and their families."  
 Am. J. Hum. Genet. 62:1361-1369(1998).  
 [11]  
 VARIANTS AGS HIS-79; THR-127; ARG-129; LEU-163; GLY-184; SER-187;  
 GLY-229; PHE-284; CYS-288; PHE-438; SER-731 AND ARG-740.  
 MEDLINE=99238889; PubMed=1020506;  
 RA Crosnier C., Briancourt C., Raynaud N., Dhorne-Pollet S., Pollet N.,  
 Bernard O., Hachouel M., Meunier-Rotival M.;  
 "Mutations in JAGGED1 gene are predominantly sporadic in Alagille  
 syndrome."  
 RT Gastroenterology 116:1141-1148(1999).  
 [12]  
 VARIANTS AGS THR-152 AND LEU-184.  
 MEDLINE=20004539; PubMed=10533065;  
 RA Filia G., Uda M., Macis D., Frau F., Crisponi L., Balli F.,  
 Barbera C., Colombo C., Frediani T., Gatti R., Iorio R., Marazzi M.G.,  
 Marcellini M., Musumeci S., Nebbia G., Vajro P., Ruffa G., Zancan L.,  
 Cao A., Devirgilis S.;  
 "Jagged-1 mutation analysis in Italian Alagille syndrome patients."  
 Hum. Mutat. 14:394-400(1999).  
 [13]  
 VARIANTS AGS TYR-229 AND ARG-386.  
 MEDLINE=20514559; PubMed=11058898;  
 RA Heritage M.L., MacMillan J.C., Colliton R.P., Genin A., Spinner N.B.,  
 Anderson G.J.;  
 "Jagged1 (JAG1) mutation detection in an Australian Alagille syndrome  
 population."  
 Hum. Mutat. 16:408-416(2000).  
 [14]  
 VARIANT TOF ASP-274.  
 MEDLINE=21067871; PubMed=11152664;  
 RA Eldadah Z.A., Hamosh A., Biery N.J., Montgomery R.A., Duke M.,  
 Elkins R., Dietz H.C.;  
 "Familial Tetralogy of Fallot caused by mutation in the jagged1  
 gene."  
 Hum. Mol. Genet. 10:163-169(2001).  
 [15]  
 VARIANT AGS SER-37.  
 MEDLINE=21096916; PubMed=11157803;  
 RA Morissette J.D., Colliton R.P., Spinner N.B.;  
 "Defective intracellular transport and processing of JAG1 missense  
 mutations in Alagille syndrome."  
 Hum. Mol. Genet. 10:405-413(2001).  
 [16]  
 VARIANTS AGS PHE-220 AND ARG-753.  
 MEDLINE=20579880; PubMed=11139247;  
 RA Crosnier C., Briancourt C., Raynaud N., Hachouel M.,  
 Meunier-Rotival M.;  
 "Fifteen novel mutations in the JAGGED1 gene of patients with Alagille  
 syndrome."  
 Hum. Mutat. 17:72-73(2001).  
 CC -!- FUNCTION: Ligand for multiple Notch receptors and involved in the  
 CC mediation of Notch signaling. May be involved in cell-fate  
 CC decisions during hematopoiesis. Seems to be involved in early  
 CC and late stages of mammalian cardiovascular development. Inhibits  
 CC myoblast differentiation (By similarity). Enhances fibroblast  
 CC growth factor-induced angiogenesis (in vitro).  
 CC -!- SUBUNIT: Interacts with NOTCH1, NOTCH2 AND NOTCH3 (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -!- TISSUE SPECIFICITY: Widely expressed in adult and fetal tissues.  
 CC In cervix epithelium expressed in undifferentiated subcolumnar  
 CC reserve cells and squamous metaplasia. Expression is up-regulated  
 CC in cervical squamous cell carcinoma. Expressed in bone marrow cell  
 CC line HS-27a which supports the long-term maintenance of immature  
 CC progenitor cells.  
 CC -!- DEVELOPMENTAL STAGE: Expressed in 32-52 days embryos in the distal  
 CC cardiac outflow tract and pulmonary artery, major arteries, portal  
 CC vein, optic vesicle, otocyst, branchial arches, metanephros,  
 CC pancreas, mesocardium, around the major bronchial branches, and in  
 CC the neural tube.  
 CC -!- DISEASE: Defects in JAG1 are the cause of Alagille syndrome (AGS)  
 CC [MIM:118450]. AGS is an autosomal dominant developmental disorder

that affects structures in the liver, heart, skeleton, eye, kidney and other organs.

-I- DISEASE: Defects in JAG1 are a cause of tetralogy of Fallot (TOF) [MIM:187500]. TOF is a congenital heart anomaly which consists of pulmonary stenosis, ventricular septal defect, dextroposition of the aorta (aorta is on the right side instead of the left) and hypertrophy of the right ventricle. This condition results in a blue baby at birth due to inadequate oxygenation. Surgical correction is emergent.

-I- SIMILARITY: Contains 15 EGF-like domains.

-I- SIMILARITY: Contains 1 DSL domain.

-I- CAUTION: Ref.7 sequence differs from that shown due to a frameshift in position 1187.

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Query Match 35.4%; Score 43.5; DB 1; Length 1218;  
Best Local Similarity 44.4%; Pred. No. 75;  
Matches 8; Conservative 2; Mismatches 5; Indels 3; Gaps 1;

3 WRCLIPA---CRNHKK 17

|||||

1081 WICCLVTFYWCLRKRRK 1098

SULT 31

PS\_BUCBP

ACPS\_BUCBP STANDARD; PRT; 128 AA.

P59475;

10-OCT-2003 (Rel. 42, Created)

10-OCT-2003 (Rel. 42, Last sequence update)

10-OCT-2003 (Rel. 42, Last annotation update)

Holo-[acyl-carrier protein] synthase (EC 2.7.8.7) (Holo-ACP synthase)

(4'-phosphopantetheinyl transferase acps).

ACPS OR BP237.

Buchnera aphidicola (subsp. Baizongia pistaciae).

Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

Enterobacteriaceae; Buchnera.

NCBI\_TaxID=135842;

[1]

SEQUENCE FROM N.A.

MEDLINE=22426901; PubMed=12522265;

Van Ham R.C.H.J., Kamerbeek J., Palacios C., Rausell C., Abascal F.,

Bastolla U., Fernandez J.M., Jimenez L., Postigo M., Silva F.J.,

Tanames J., Viguera E., Latorre A., Valencia A., Moran F., Moya A.,

"Reductive genome evolution in Buchnera aphidicola";

Proc. Natl. Acad. Sci. U.S.A. 100:581-586(2003).

-I- FUNCTION: Transfers the 4'-phosphopantetheine moiety from coenzyme

A to a Ser of acyl-carrier protein (By similarity).

-I- CATALYTIC ACTIVITY: CoA + apo-[acyl-carrier protein] = adenosine

3',5'-bisphosphate + holo-[acyl-carrier protein].

-I- COFACTOR: Magnesium (By similarity).

-I- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

-I- SIMILARITY: Belongs to the P-Pant transferase superfamily. Acps

family.

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EMBL; AB014016; AAC026964.1; -

HAMAP; MF\_00101; -; 1.

InterPro; IPR008278; 4-PPT transf.

InterPro; IPR002582; ACPS.

InterPro; IPR004568; Pantethn\_trn.

Pfam; PF01648; ACPS; 1.

TIGRFAMs; TIGR00516; acps; 1.

TIGRFAMs; TIGR00556; pantethn\_trn; 1.

Transferase; Lipid synthesis; pantethin; Fatty acid biosynthesis; Magnesium;

KW Complete proteome.  
FT METAL 9  
FT METAL 60  
SQ SEQUENCE 128 AA; 14502 MW; 5ED8856BE07DDEDA CRC64;

Query Match 35.0%; Score 43; DB 1; Length 128;

Best Local Similarity 35.3%; Pred. No. 10;

Matches 6; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 2 NWRCLIPACRNHHKPF 18

|||

Db 35 NYELNLEPCKQNYTKF 51

RESULT 32

FOL1\_BOVIN

ID FOL1\_BOVIN STANDARD; PRT; 222 AA.

AC P02702;

DT 21-JUL-1986 (Rel. 01, Created)

DT 23-OCT-1986 (Rel. 02, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Milk folate-binding protein (FBP) (Folate receptor alpha).

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC Bovidae; Bovinae; Bos.

OX NCBI\_TaxID=9913;

RN [1]

RP SEQUENCE.

RC TISSUE=Milk;

RA Svendsen I., Hansen S.I., Holm J., Lyngbye J.;

RT "The complete amino acid sequence of the folate-binding protein from

cow's milk";

RL Carlsberg Res. Commun. 49:123-131(1984).

RN [2]

RP SEQUENCE OF 1-62; 72-102 AND 192-222.

RC TISSUE=Milk;

RA Svendsen I., Martin B., Pedersen T.G., Hansen S.I., Holm J.;

RT Lyngbye J.;

RT "Isolation and characterization of the folate-binding protein from

cow's milk";

RL Carlsberg Res. Commun. 44:89-99(1979).

CC -I- FUNCTION: Binds to folate and reduced folic acid derivatives and

mediates delivery of 5-methyltetrahydrofolate to the interior of

cells.

CC -I- PTM: Eight disulfide bonds are present.

CC -I- SIMILARITY: Belongs to the folate receptor family.

DR PIR; A03161; BFBO.

DR InterPro; IPR004269; Folt\_chemrecept.

DR Pfam; PF03024; Folate\_rec; 1.

KW Receptor; Glycoprotein; Milk; Folate-binding.

FT CARBOHYD 49 49 N-LINKED (GLCNAC. .).

FT CARBOHYD 141 141 N-LINKED (GLCNAC. .).

SQ SEQUENCE 222 AA; 25825 MW; 528C388E9AC0484 CRC64;

Query Match 35.0%; Score 43; DB 1; Length 222;

Best Local Similarity 50.0%; Pred. No. 18;

Matches 8; Conservative 3; Mismatches 3; Indels 2; Gaps 1;

QY 1 FNRWCC--LIPACREN 14

|||||

Db 64 FNRWCC--LIPACREN 79

RESULT 33

YAT6\_RHOBL

ID YAT6\_RHOBL STANDARD; PRT; 249 AA.

AC P05449; C05939;

DT 01-NOV-1988 (Rel. 09, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

OS ATP synthase subunits region ORF 6.

OS Rhodospseudomonas blattica.



SULT 35

15 \_CG15 ARATH STANDARD; PRT; 678 AA.  
 Q9SL29;  
 15-MAR-2004 (Rel. 43, Created)  
 15-MAR-2004 (Rel. 43, Last sequence update)  
 15-MAR-2004 (Rel. 43, Last annotation update)  
 Putative cyclic nucleotide-gated ion channel 15 (cyclic nucleotide-  
 and calmodulin-regulated ion channel 15).  
 CNGC15 OR AT2G28260 OR T3B23.7.  
 Arabidopsis thaliana (Mouse-ear cress).  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 eurosid II; Brassicales; Brassicaceae; Arabidopsids.  
 NCBI\_TaxId=3702;  
 [1]  
 SEQUENCE FROM N.A.  
 STRAIN=cv. Columbia;  
 MEDLINE=20083487; PubMed=10617197;  
 Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,  
 Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblum T.V.,  
 Buell C.R., Ketchum K.A., Lee J.J., Renning C.M., Koo H.L.,  
 Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L.,  
 Tallon L.J., Gill J.E., Adams M.D., Cartera A.J., Creasy T.H.,  
 Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,  
 Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,  
 Venter J.C.;  
 "Sequence and analysis of chromosome 2 of the plant Arabidopsis  
 thaliana.";  
 Nature 402:761-768(1999).  
 [2]  
 GENE FAMILY, AND NOMENCLATURE.  
 MEDLINE=21392307; PubMed=11500563;  
 Maeser P., Thomine S., Schroeder J.I., Ward J.M., Hirsch K., Sze H.,  
 Talke I.N., Antmann A., Maathuis F.J.M., Sanders D., Harper J.F.,  
 Tchieu J., Gribskov M., Persans M.W., Salt D.E., Kim S.A.,  
 Gueriot M.B.;  
 "Phylogenetic relationships within cation transporter families of  
 Arabidopsis.";  
 Plant Physiol. 126:1646-1667(2001).  
 -!- FUNCTION: Putative cyclic nucleotide-gated ion channel.  
 -!- SUBUNIT: Homotrimer or heterotrimer (Potential).  
 -!- SUBCELLULAR LOCATION: Integral membrane protein. Plasma membrane  
 (Potential).  
 -!- DOMAIN: The binding of calmodulin to the C-terminus might  
 interfere with cyclic nucleotide binding and thus channel  
 activation (By similarity).  
 -!- SIMILARITY: Belongs to the cyclic nucleotide-gated cation channel  
 (TC 1.A.1.5) family.  
 -!- SIMILARITY: Contains 1 cyclic nucleotide-binding domain.  
 -!- SIMILARITY: Contains 1 IQ domain.  
 -----  
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 -----  
 EMBL; AC006202; AAD29827.1; -;  
 PIR; G84682; G84682.  
 InterPro; IPR000595; CNMP binding.  
 InterPro; IPR005821; Ion\_Trans.  
 InterPro; IPR000048; IQ\_region.  
 InterPro; IPR01622; K-channel\_pore.  
 Pfam; PF00027; CNMP binding; 1.  
 Pfam; PF00520; ion\_trans; 1.  
 Pfam; PF00612; IQ; 1.  
 SMART; SM00100; CNMP; 1.  
 PROSITE; PS00888; CNMP BINDING 1; FALSE\_NEG.  
 PROSITE; PS00889; CNMP BINDING 2; FALSE\_NEG.  
 PROSITE; PS00042; CNMP BINDING 3; 1.

DR PROSITE; PS00096; IQ; 1.  
 KW Hypothetical protein; Ion transport; Ionic channel;  
 KW Calmodulin-binding; cAMP-binding; cGMP-binding; Transmembrane;  
 KW Multigene family.  
 FT DOMAIN 1 81 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 82 102 H1 (POTENTIAL).  
 FT DOMAIN 103 115 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 116 136 H2 (POTENTIAL).  
 FT DOMAIN 137 170 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 171 191 H3 (POTENTIAL).  
 FT DOMAIN 192 203 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 204 224 H4 (POTENTIAL).  
 FT DOMAIN 225 245 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 246 266 H5 (POTENTIAL).  
 FT DOMAIN 267 364 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 365 385 H6 (POTENTIAL).  
 FT DOMAIN 386 678 CYTOPLASMIC (POTENTIAL).  
 FT NP\_BIND 471 595 CNMP.  
 FT BINDING 542 542 CAMP OR CGMP (BY SIMILARITY).  
 FT DOMAIN 587 602 CALMODULIN-BINDING (BY SIMILARITY).  
 FT DOMAIN 607 638 IQ.  
 SQ SEQUENCE 678 AA; 78722 MW; E020D14E44050B64 CRC64;  
 Query Match 35.0%; Score 43; DB 1; Length 678;  
 Best Local Similarity 46.7%; Pred. No. 51;  
 Matches 7; Conservative 1; Mismatches 7; Indels 0; Gaps 0;  
 QY 3 WRCLIPACRRNKK 17  
 DB 609 WAACFIQAWRRHRK 623

Search completed: February 18, 2004, 06:07:09

Job time : 48 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

protein - protein search, using sw model

on: February 18, 2004, 06:03:18 ; Search time 80 Seconds  
(without alignments)  
74.936 Million cell updates/sec

le: US-09-806-376-1

fect score: 123

uence: 1 FNRCCILIPACRRNHKKFC 19

ring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

arched: 1017041 seqs, 315518202 residues

al number of hits satisfying chosen parameters: 1017041

imum DB seq length: 0

imum DB seq length: 2000000000

it-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

abase :

SPTREMBL\_25:\*

1: sp\_archaea:\*

2: sp\_bacteria:\*

3: sp\_fungi:\*

4: sp\_human:\*

5: sp\_invertebrate:\*

6: sp\_mammal:\*

7: sp\_mhc:\*

8: sp\_organelle:\*

9: sp\_phage:\*

10: sp\_plant:\*

11: sp\_rodent:\*

12: sp\_virus:\*

13: sp\_vertebrate:\*

14: sp\_unclassified:\*

15: sp\_rvirus:\*

16: sp\_bacteriaph:\*

17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

sult	No.	Score	Query Match	Length	DB	ID	Description
1	52	42.3	189	5	Q17888	Q17888 caenorhabdi	
2	51	41.5	328	8	Q8HRP0	Q8hrp0 dipterogium	
3	50.5	41.1	720	5	O01605	O01605 caenorhabdi	
4	49	39.8	82	12	O39626	O39626 cydia pomon	
5	49	39.8	180	2	Q7X4R1	Q7x4r1 streptomyc	
6	49	39.8	188	16	Q8Y300	Q8y300 ralsstonia s	
7	49	39.8	334	16	Q8X299	Q8x299 ralsstonia s	
8	49	39.8	610	4	Q9NRE9	Q9nre9 homo sapien	
9	49	39.8	640	10	Q96397	Q96397 chlamydomon	
10	48.5	39.4	534	11	Q8BLN2	Q8bln2 mus musculu	
11	48	39.0	141	5	Q7YX40	Q7yx40 caenorhabdi	
12	48	39.0	145	16	Q8FK43	Q8fk43 escherichia	
13	48	39.0	338	4	Q9UJ42	Q9uj42 homo sapien	
14	48	39.0	510	4	Q9H846	Q9h846 homo sapien	
15	48	39.0	510	4	Q96GM8	Q96gm8 homo sapien	
16	48	39.0	510	4	Q81WN5	Q81wn5 homo sapien	

17	48	39.0	636	11	Q8K2J3	Q8K2J3 mus musculu
18	48	39.0	5322	5	Q9VPL9	Q9VPL9 drosophila
19	47	38.2	105	4	Q9NP04	Q9NP04 homo sapien
20	47	38.2	283	2	Q9K508	Q9K508 pseudomonas
21	46.5	37.8	46	11	Q64412	Q64412 cavia porce
22	46	37.4	24	6	Q28428	Q28428 gorilla gor
23	46	37.4	40	5	Q86RB2	Q86RB2 conus geogr
24	46	37.4	125	9	Q854F9	Q854F9 mycobacteri
25	46	37.4	174	10	O81217	O81217 zea mays (m
26	46	37.4	314	5	Q965R6	Q965R6 caenorhabdi
27	46	37.4	363	12	Q69275	Q69275 equine herp
28	46	37.4	401	12	Q8V723	Q8V723 simian herp
29	46	37.4	401	12	Q7T5C2	Q7T5C2 simian herp
30	46	37.4	1236	11	Q91YB6	Q91YB6 rattus norv
31	45.5	37.0	97	3	Q04923	Q04923 saccharomyc
32	45	37.0	350	17	Q8TN25	Q8TN25 methanosarc
33	45	36.6	28	13	O42558	O42558 brachydanio
34	45	36.6	237	11	Q9JMF2	Q9JMF2 mus musculu
35	45	36.6	249	6	Q9XSH1	Q9XSH1 sus scrofa
36	45	36.6	361	16	O53533	O53533 mycobacteri
37	45	36.6	361	16	Q7VEM6	Q7VEM6 mycobacteri
38	45	36.6	413	4	Q9H8S1	Q9H8S1 homo sapien
39	45	36.6	429	5	Q8MYQ9	Q8MYQ9 caenorhabdi
40	45	36.6	749	10	Q38743	Q38743 antirrhinum
41	45	36.6	2644	4	Q13535	Q13535 homo sapien
42	44.5	36.2	97	5	Q8WPU0	Q8WPU0 trypanosoma
43	44.5	36.2	2561	5	O46025	O46025 caenorhabdi
44	44.5	36.2	4498	13	O93291	O93291 fugu rubrip
45	44	35.8	48	6	Q8WME4	Q8WME4 desmodus ro
46	44	35.8	48	6	Q8WNZ5	Q8WNZ5 moroneus me
47	44	35.8	55	11	Q9WJN4	Q9WJN4 rattus norv
48	44	35.8	123	16	Q7TXR1	Q7TXR1 mycobacteri
49	44	35.8	125	16	Q8XM87	Q8XM87 clostridium
50	44	35.8	129	12	Q91CZ3	Q91CZ3 tt virus. O

#### ALIGNMENTS

#### RESULT 1

Q17888	PRELIMINARY;	PRT; 189 AA.
AC Q17888		
DT 01-NOV-1996 (TrEMBLrel. 01, Created)		
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)		
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)		
DE Hypothetical protein.		
GN Cl0A4.6.		
OS Caenorhabditis elegans.		
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;		
OC Rhabditidae; Pelodierinae; Caenorhabditis.		
OX NCBI_TaxID=6239;		
RN [1]		
RP SEQUENCE FROM N.A.		
RC STRAIN=Bristol N2;		
RX MEDLINE=99069613; PubMed=9851916;		
RA None;		
RT "Genome sequence of the nematode C. elegans: a platform for		
RL investigating biology. The C. elegans Sequencing Consortium."		
RN [2]		
RP SEQUENCE FROM N.A.		
RC STRAIN=Bristol N2;		
RA Pauley A.;		
RT "The sequence of C. elegans cosmid Cl0A4.";		
RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.		
RN [3]		
RP SEQUENCE FROM N.A.		
RC STRAIN=Bristol N2;		
RA Waterston R.;		
RT "Direct Submission";		
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.		
DR EMBL; U23454; AAC46520.1; -.		

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PIR; TL5479; TL5479.
wormPep; C10A4.6; CE02474.
Hypothetical protein.
SEQUENCE 169 AA; 22250 MW; 218F93C56EC773CE CRC64;

Query Match 42.3%; Score 52; DB 5; Length 189;
Best Local Similarity 44.4%; Pred. No. 1.6;
Matches 12; Conservative 1; Mismatches 4; Indels 10; Gaps 1;

1 FNWRCCLIPLA-----CRNHKK 17
|||
144 FNRCCQCATKMKLMNQICRRNGK 170
|||

MULT 2
RPO QSHRPO PRELIMINARY; PRT; 328 AA.
QSHRPO;
01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
NADH dehydrogenase subunit F (fragment).
NDHF.
Dipterygium glaucum.
Chloroplast.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Dipterygium.
NCBI_TaxID=202664;
[1]
SEQUENCE FROM N.A.
Hall J.C., Sytsma K.J., Iltis H.H.;
"Phylogeny of Caparraceae and Brassicaceae based on chloroplast
sequence data.";
Am. J. Bot. 89:1826-1842(2002).
EMBL; AY123292; AM82796.1; -.
GO; GO:0009507; C:chloroplast; IEA.
GO; GO:0008137; C:NADH dehydrogenase (ubiquinone) activity; IEA.
GO; GO:0006120; P:mitochondrial electron transport, NADH to u. .; IEA.
InterPro; IPR001750; Oxidored_q1.
InterPro; IPR002128; Oxidored_q1.
Pfam; PF00361; oxidored_q1; 1-1_C.
Pfam; PF01010; oxidored_q1_C; 1.
Chloroplast.
NON_TER 1
NON_TER 328
SEQUENCE 328 AA; 37788 MW; 64E91EC91874E793 CRC64;

Query Match 41.5%; Score 51; DB 8; Length 328;
Best Local Similarity 50.0%; Pred. No. 3.7;
Matches 11; Conservative 1; Mismatches 6; Indels 4; Gaps 1;

2 FNWRCCLIPLACRHHK----FC 19
|||
126 NNFNCLVPLLRNHKKRVSFC 147
|||

MULT 3
1605 Q01605 PRELIMINARY; PRT; 720 AA.
Q01605;
01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
[1]
SEQUENCE FROM N.A.
STRAIN=Bristol N2;

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RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
[2]
RN SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Greco T., Hawkins M.;
RT "The sequence of C. elegans cosmid T10E9.";
RL submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
[3]
RN SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RT "Direct Submission.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; U97403; AAB52470.1; -.
DR PIR; T25883; T25883.
DR WormPep; T10E9.2; CE13545.
KW Hypothetical protein.
SQ SEQUENCE 720 AA; 83989 MW; 9A6D9E8B3E55E05 CRC64;

Query Match 41.1%; Score 50.5; DB 5; Length 720;
Best Local Similarity 60.0%; Pred. No. 8.7;
Matches 9; Conservative 0; Mismatches 3; Indels 3; Gaps 1;

QY 1 FNWRCCLIPLACRHH 15
|||
DB 347 FNWRCCLIPLACRHH 358
|||

RESULT 4
O39626 PRELIMINARY; PRT; 82 AA.
AC O39626;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE ORF353A (ORF42 similar to XcGV ORF36).
OS ORF42.
OS Cydia pomonella granulosis virus (CpGV) (Cydia pomonella
granulovirus).
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae; Granulovirus.
OX NCBI_TaxID=28289;
RN [1]
RP SEQUENCE FROM N.A.
RA Jehle J.A., van der Linden I.F.A., Vlask J.M.;
RT "Identification and sequence analysis of the integration site of
transposon TcP3.2 in the genome of Cydia pomonella granulovirus.";
RL Virus Res. 0:0-0(1997).
[2]
RN SEQUENCE FROM N.A.
RC STRAIN=Mexican 1;
RX MEDLINE=93188168; PubMed=8445726;
RA Crook N.E., Clem R.J., Miller L.K.;
RT "An apoptosis-inhibiting baculovirus gene with a zinc finger-like
motif.";
RL J. Virol. 67:2168-2174 (1993).
[3]
RN SEQUENCE FROM N.A.
RC STRAIN=Mexican 1;
RX MEDLINE=96207404; PubMed=8615018;
RA Theilmann D.A., Chantler J.K., Stewart S., Flippen H.T., Vlask J.M.,
Crook N.E.;
RT "Characterization of a highly conserved baculovirus structural protein
that is specific for occlusion-derived virions.";
RL Virology 218:148-158(1996).
[4]
RN SEQUENCE FROM N.A.
RC STRAIN=Mexican 1;
RX MEDLINE=97380577; PubMed=9237352;
RA Kang W., Crook N.E., Winstanley D., O'Reilly D.R.;

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SEQUENCE 334 AA; 35204 MW; 0FC0176E32E8F3BA2 CRC64;
Query Match 39.8%; Score 49; DB 16; Length 334;
Best Local Similarity 41.2%; Pred. No. 7.8;
Matches 7; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

3 WRCCLIPACRRNHKKFC 19
89 WSCGTCTPCRRDQENLC 105

SULT 8
Q9NRE9 PRELIMINARY; PRT; 610 AA.
Q9NRE9;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Cone photoreceptor cGMP-gated cation channel beta-subunit.
CNGB3.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
TISSUE=Retina;
MEDLINE=20347712; PubMed=10888875;
Sundin O.H., Yang J.-M., Li Y., Zhu D., Hurd J.N., Mitchell T.H.,
Silva E.D., Maumenee I.H.;
"Genetic basis of total colourblindness among the Pingelapese
islanders.";
Nat. Genet. 25:289-293(2000).
EMBL; AF228520; RA080179.1; -.
GO; GO:0007601; P:vision; TAS.
InterPro; IPR000595; cNMP_binding.
InterPro; IPR005821; Ion_trans.
InterPro; IPR001622; K-channel_pore.
Pfam; PF00027; cNMP_binding; 1.
Pfam; PF00520; ion_trans; 1.
SMART; SM00100; cNMP; 1.
PROSITE; PS00888; cNMP_BINDING_1; 1.
PROSITE; PS00042; cNMP_BINDING_3; 1.
Ionic channel; Receptor; Transmembrane.
SEQUENCE 610 AA; 70039 MW; 843B01F12643B73A CRC64;

Query Match 39.8%; Score 49; DB 4; Length 610;
Best Local Similarity 66.7%; Pred. No. 13;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

1 FNRCCCLIP 9
35 YNWNCCFIP 43

SULT 9
Q96397 PRELIMINARY; PRT; 640 AA.
Q96397; O04833; O04733;
01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
LKG5.
LKG5.
Chlamydomonas reinhardtii.
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Voivocales;
Chlamydomonadaceae; Chlamydomonas.
NCBI_TaxID=3055;
[1]
SEQUENCE FROM N.A.
Gloeckner G., Beck C.F.;
Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
[2]

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RP SEQUENCE FROM N.A.
RA Gloeckner G., Beck C.F.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U73817; AB17561.1; -.
DR EMBL; U73818; AB39840.1; -.
DR PIR; T08179; T08179.
DR InterPro; IPR001007; VWF_C.
DR PROSITE; PS01208; VWF_C_1.
SQ SEQUENCE 640 AA; 67298 MW; 764BEE7ADC32FC99 CRC64;

Query Match 39.8%; Score 49; DB 10; Length 640;
Best Local Similarity 60.0%; Pred. No. 14;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 NWRCCCLIPAC 11
DB 586 NWCCCLPGC 595

RESULT 10
Q8BLN2 PRELIMINARY; PRT; 534 AA.
ID Q8BLN2;
AC Q8BLN2;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Weakly similar to kinesin heavy chain-like protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cortex;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK044049; BAC31752.1; -.
FT NON_TER
SQ SEQUENCE 534 AA; 58612 MW; 71AD5390D8D7322F CRC64;

Query Match 39.4%; Score 48.5; DB 11; Length 534;
Best Local Similarity 40.9%; Pred. No. 14;
Matches 9; Conservative 3; Mismatches 3; Indels 7; Gaps 1;

QY 2 NW-----RCCLIPACRRNHK 16
DB 512 NWKLSSTLNRCCLVYHPRHE 533

RESULT 11
Q7YX40 PRELIMINARY; PRT; 141 AA.
ID Q7YX40;
AC Q7YX40;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein F36G3.3.
GN F36G3.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Feloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RA "Genome sequence of the nematode C.elegans: A platform for
RT investigating biology.";

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Science 282:2012-2018(1998).
[2]
SEQUENCE FROM N.A.
STRAIN=Bristol N2;
White S.;
Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
EMBL; 247069; CAB17781.1; -.
Hypothetical protein.
SEQUENCE 141 AA; 15967 MW; 24E55561B1EBD95B CRC64;

Query Match 39.0%; Score 48; DB 5; Length 141;
Best Local Similarity 50.0%; Pred. No. 5.4; Indels 0; Gaps 0;
atches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

3 WRCCFLPACRRNHK 16
|||||:|||||
109 WCCCFLPCLRSCK 122

ULT 12
K43 Q8FK43 PRELIMINARY; PRT; 145 AA.
Q8FK43;
01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein ypci.
YBCI OR C0643.
Escherichia coli O6.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
NCBI_TaxID=217992;
[1]
SEQUENCE FROM N.A.
STRAIN=O6:H1 / CFT073 / ATCC 700928;
MEDLINE=22388234; PubMed=12471157;
Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
"Extensive mosaic structure revealed by the complete genome sequence
of uropathogenic Escherichia coli.";
Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
EMBL; AE016757; AA079120.1; -.
InterPro; IPR007404; DUF457.
Pfam; PF04307; DUF457; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 145 AA; 16877 MW; 1004E10029242686 CRC64;

Query Match 39.0%; Score 48; DB 16; Length 145;
Best Local Similarity 58.3%; Pred. No. 5.5;
atches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

2 NWRCCLPACRR 13
|||||:|||||
5 SWRCCLPMTYR 16

ULT 13
J342 Q9UJ42 PRELIMINARY; PRT; 338 AA.
Q9UJ42;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Putative G-protein coupled receptor.
GPCR150 OR GPCR.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
TISSUE=Pancreas;
Conklin D., Yee D., Engelbrecht J., Vissing H.;
"Mining of Assembled EST Data in Protein Super families: Application
to the G Protein-Coupled Receptors.";
Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
[2]
RN SEQUENCE FROM N.A.
RP TISSUE=Cervix;
RA Strausberg R.;
Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
[3]
RN SEQUENCE FROM N.A.
RP Takeda S., Kadowaki S., Haga T., Takasu H., Mitaku S.;
"Identification of G protein-coupled receptor genes from the human
genome sequence.";
RN Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ249248; CAB55314.1; -.
DR EMBL; BC000181; AA00181.1; -.
DR EMBL; AB083583; BAB89296.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR Rhodpsn.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 338 AA; 39786 MW; 50B38F90E0311175 CRC64;

Query Match 39.0%; Score 48; DB 4; Length 338;
Best Local Similarity 75.0%; Pred. No. 11;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 NWRCCCLIP 9
|||||:|||||
DB 313 NWRCCCFIP 320

RESULT 14
Q9H846 PRELIMINARY; PRT; 510 AA.
AC Q9H846;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein FLJ13949.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RP Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
RA Wagatsuma M., Hosoi T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura K., Nagahara K., Masuno Y.,
RA Nimomiya K., Iwayanagi T.;
"NEDO human cDNA sequencing project.";
RN Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
RL EMBL; AK024011; BAB14774.1; -.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR InterPro; IPR006941; CAP1.
DR InterPro; IPR000571; Znf_CCCH.
DR Pfam; PF04857; CAP1; 1.
DR Pfam; PF00642; zf-CCCH; 1.
KW Hypothetical protein.
SQ SEQUENCE 510 AA; 56566 MW; FFA612937B012252 CRC64;

Query Match 39.0%; Score 48; DB 4; Length 510;
Best Local Similarity 57.1%; Pred. No. 16;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

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2 NWRCLIPACRRNH 15
:|||||
282 DYRCCLPPATHRPH 295

ULT 15
GNM8
Q96GM8 PRELIMINARY; PRT; 510 AA.
Q96GM8;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
TISUB=Uterus;
Strausberg R.;
Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
EMBL; BC009364; AA09364.1; -.
Genew; HGNC:15954; TOE1.
GO; GO:0003676; P:nucleic acid binding; IEA.
InterPro; IPR006941; CAF1.
InterPro; IPR000571; Znf_CCH.
Pfam; PF04857; CAF1; 1.
Pfam; PF00642; zf-CCCH; 1.
Hypothetical protein.
SEQUENCE 510 AA; 56547 MW; 584616F50E12929 CRC64;

Query Match 39.0%; Score 48; DB 4; Length 510;
Best Local Similarity 57.1%; Pred. No. 16;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

2 NWRCLIPACRRNH 15
:|||||
282 DYRCCLPPATHRPH 295

ULT 16
WN5
Q81WN5 PRELIMINARY; PRT; 510 AA.
Q81WN5;
01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Target of Egr1 protein.
TOE1.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
de Belle I., Wu J.-X., Sperandio S., Mercola D., Adamson E.D.;
"In vivo cloning and characterization of a new growth suppressor
protein TOE1 as a direct target of Egr1."
Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
EMBL; AV169960; AAN75441.1; -.
GO; GO:0003676; P:nucleic acid binding; IEA.
InterPro; IPR006941; CAF1.
InterPro; IPR000571; Znf_CCH.
Pfam; PF04857; CAF1; 1.
Pfam; PF00642; zf-CCCH; 1.
SEQUENCE 510 AA; 56489 MW; E3D616F59C2E2A85 CRC64;

Query Match 39.0%; Score 48; DB 4; Length 510;
Best Local Similarity 57.1%; Pred. No. 16;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

2 NWRCLIPACRRNH 15
:|||||
282 DYRCCLPPATHRPH 295

Db 282 DYRCCLPPATHRPH 295
:|||||
PRELIMINARY; PRT; 636 AA.
Q8K2J3
AC Q8K2J3;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC031207; AAH31207.1; -.
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 636 AA; 72242 MW; 3C5C72EACACEFE055 CRC64;

Query Match 39.0%; Score 48; DB 11; Length 636;
Best Local Similarity 52.9%; Pred. No. 20;
Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 FNRCLIPACRRNHK 17
:|||||
DB 496 FDKCLPPAGVENYK 512
:|||||

RESULT 18
Q9VPL9 PRELIMINARY; PRT; 5322 AA.
AC Q9VPL9; Q9NI64;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE CG3696 protein (KISMET-L long isoform).
GN KIS OR CG3660 OR CG3696 OR CG18326.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Ephydroidea; Endopterygota; Diptera; Brachycera; Muscomorpha.
CX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
RA Brandon R.C., Rogers J.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hosain D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

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Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., Merkulov G., Milshina N.V., Mobarri J., Morris J., Moshrefi A., Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Siden-Kiamos I., Simpson M.K., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J., Williams S.M., Woodgate T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 "The genome sequence of *Drosophila melanogaster*";  
 Science 287:2185-2195(2000).  
 [2]  
 SEQUENCE FROM N.A.  
 Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A., Evans C.A., Gocayne J.D., Ananatzides P.G., Brandon R.C., Rogers Y., Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A., Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M., Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D., Ferreira S., Frise B., Galle R.F., Garg N.S., George R.A., Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J., Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A., McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J., Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B., Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F., Stapleton M., Strong R., Svirkas R., Tector C., Tyler D., Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;  
 "Sequencing of *Drosophila melanogaster* genome";  
 Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 [3]  
 SEQUENCE FROM N.A.  
 Misra S., Creeby M.A., Matthews B.B., Bayraktaroglu L., Campbell K., Hradecky P., Huang Y., Kaminker J.S., Prochink S.E., Smith C.D., Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E., Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N., Kronmiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;  
 "Annotation of *Drosophila melanogaster* genome";  
 Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 [4]  
 SEQUENCE FROM N.A.  
 Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;  
 Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 [5]  
 SEQUENCE FROM N.A.  
 FlyBase;  
 Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
 [6]  
 SEQUENCE FROM N.A.  
 Therrien M., Morrison D.K., Wong A.M., Rubin G.M.;  
 "A Genetic Screen for Modifiers of a KR-Dependent Rough Eye Phenotype in *Drosophila*";  
 Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
 EMBL; AF003590; AAF51527.3; -;  
 EMBL; AF215703; AAF43004.1; -;  
 HSPB; P23197; IAP0.  
 FlyBase; FBgn001309; kis.  
 GO; GO:0000785; C:nucleus; IEA.  
 GO; GO:0005634; C:nucleus; IEA.  
 GO; GO:0005524; F:ATP binding; IEA.  
 GO; GO:0008026; F:ATP dependent helicase activity; IEA.  
 GO; GO:0003682; F:chromatin binding; IEA.  
 GO; GO:0016787; F:hydrolase activity; IEA.  
 GO; GO:0006333; P:chromatin assembly/disassembly; IEA.  
 InterPro; IPR000953; Chromo.  
 InterPro; IPR001410; DEAD.  
 InterPro; IPR001650; Helicase\_C.

DR InterPro; IPR000330; SNF2\_N.  
 DR Pfam; PF00385; Chromo; 1.  
 DR Pfam; PF00271; helicase\_C; 1.  
 DR Pfam; PF00176; SNF2\_N; 1.  
 DR SMART; SM00298; CHROMO; 2.  
 DR SMART; SM00487; DEXDC; 1.  
 DR SMART; SM00490; HELIC; 1.  
 DR PROSITE; PSS0013; CHROMO\_2; 1.  
 KW ATP-binding; Helicase; Hydrolase.  
 SQ SEQUENCE 5322 AA; 573615 MW; C9608375FA71C211 CRC64;  
 Query Match 39.0%; Score 48; DB 5; Length 5322;  
 Best Local Similarity 42.1%; Pred. No. 1.2e+02;  
 Matches 8; Conservative 2; Mismatches 9; Indels 0; Gaps 0;  
 Qy 1 FNWRCCILIPACRRNHKKFC 19  
 Db 2158 FNWRLCVIDEAHLKRNRC 2176  
 RESULT 19  
 Q9NP04 PRELIMINARY; PRT; 105 AA.  
 AC Q9NP04  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Folate receptor alpha isoform (Fragment).  
 OS Homo sapiens (Human)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94339186; PubMed=8061055;  
 RA Prasad P.D., Ramamoorthy S., Moe A.J., Smith C.H., Leibach F.H., Ganapathy V.;  
 RT "Selective expression of the high-affinity isoform of the folate receptor (FR-alpha) in the human placental syncytiotrophoblast and chorionicarcoma cells.";  
 RL Biochim. Biophys. Acta 1223:71-75(1994).  
 DR EMBL; S73490; AAB31700.1; -;  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR InterPro; IPR004269; Folt\_chemrecept.  
 DR Pfam; PF03024; Folate\_rec; 1.  
 KW Receptor.  
 FT NON TER 105 105  
 SQ SEQUENCE 105 AA; 12225 MW; B30DE5868EFB2CE9 CRC64;  
 Query Match 38.2%; Score 47; DB 4; Length 105;  
 Best Local Similarity 50.0%; Pred. No. 6;  
 Matches 8; Conservative 3; Mismatches 3; Indels 2; Gaps 1;  
 Qy 1 FNWRCC--LIPACRRN 14  
 Db 84 FNWVHCGEAPACKRH 99  
 RESULT 20  
 Q9K508 PRELIMINARY; PRT; 283 AA.  
 AC Q9K508;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Hypothetical protein.  
 OS Pseudomonas syringae (pv. pisi).  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
 OC Pseudomonadaceae; Pseudomonas.  
 OX NCBI\_TaxID=59510;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=race 2;

Arnold D.L., Jackson R.W., Vivian A.;  
"Evidence for the mobility of an avirulence gene, *avrPp1A*, between  
the chromosome and plasmids of races of *Pseudomonas syringae* pv.  
*plasi*.";

Mol. Plant Pathol. 1:195-199(2000).

EMBL; AJ251482; CAB96973.1; -

InterPro; IPR003738; DUF159.

Pfam; PF02586; DUF159; 1.

Hypothetical protein.

SEQUENCE 283 AA; 31984 MW; 6461D7CF59A5ADDE CRC64;

Query Match 38.2%; Score 47; DB 2; Length 283;

Best Local Similarity 34.8%; Pred. No. 14;

Matches 8; Conservative 6; Mismatches 3; Indels 6; Gaps 1;

1 FNRCC-----LIPACRRNKK 17

18 FDWDCMHQLTLQACQSVRQ 40

SULT 21

1412

Q64412 PRELIMINARY; PRT; 46 AA.

01-NOV-1996 (TrEMBLrel. 01, Created)

01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

Protamine 1 (Sperm protamines P1) (Fragment).

PRM1.

Cavia porcellus (Guinea pig).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Hystriocognathi; Cavidae; Cavia.

NCBI\_TaxID=10141;

[1]

SEQUENCE FROM N.A.

Queralt R., Adroer R., Oliva R.;

"Protamine 1 cDNA and genomic sequence from the guinea pig (Cavia

porcellus) reveals marked differences to mouse and rat protamines.";

Submitted (JAN-1995) to the EMBL/GenBank/DBJ databases.

-!- FUNCTION: PROTAMINES SUBSTITUTE FOR HISTONES IN THE CHROMATIN OF

SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT

SPERM DNA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX (BY

SIMILARITY).

-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

-!- SIMILARITY: BELONGS TO THE PROTAMINE P1 FAMILY.

EMBL; M83895; AA58348.1; -

GO; GO:0005694; C:chromosome; IEA.

GO; GO:0000786; C:nucleosome; IEA.

GO; GO:0003634; C:nucleus; IEA.

GO; GO:0003677; F:DNA binding; IEA.

GO; GO:0007001; P:chromosome organization and biogenesis (gen. . .); IEA.

GO; GO:0007076; P:mitotic chromosome condensation; IEA.

GO; GO:0007283; P:spermatogenesis; IEA.

InterPro; IPR000221; Protamine P1.

Pfam; PF00260; Protamine P1.1.

PROSITE; PS00048; PROTAMINE\_P1; 1.

Chromosomal protein; DNA condensation; DNA-binding; Nuclear protein;

Nucleosome core; Spermatogenesis.

NON\_TER 46 46

SEQUENCE 46 AA; 6218 MW; BB82967CC408463D CRC64;

Query Match 37.8%; Score 46.5; DB 11; Length 46;

Best Local Similarity 42.1%; Pred. No. 3.6;

Matches 8; Conservative 4; Mismatches 4; Indels 3; Gaps 1;

3 WRCCPLPA---CRRNKKF 18

4 YRCRSPSRRCRRRRRF 22

SULT 22

3428

Q28428 PRELIMINARY; PRT; 24 AA.

Q28428;

01-NOV-1996 (TrEMBLrel. 01, Created)

01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

Relaxin (Fragment).

RLX.

OS Gorilla gorilla (gorilla).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.

NCBI\_TaxID=9593;

[1]

SEQUENCE FROM N.A.

SRPAINRG YK; Fu P., Tregear G.G.W.;

"Characterisation of primate relaxin genes.";

J. Mol. Endocrinol. 0:0-0(1993).

-!- SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY).

EMBL; Z27226; CAA81740.1; -

PIR; S42778; S42778.

HSSP; P04090; 6RLX.

GO; GO:0005576; C:extracellular; IEA.

GO; GO:0005179; F:hormone activity; IEA.

GO; GO:0007582; P:physiological processes; IEA.

InterPro; IPR004825; Ins/IGF/relax.

Pfam; PF00049; Insulin; 1.

PROSITE; PS00262; INSULIN; 1.

NON\_TER 1

SEQUENCE 24 AA; 2766 MW; 669743C18CBF5927 CRC64;

Query Match 37.4%; Score 46; DB 6; Length 24;

Best Local Similarity 43.8%; Pred. No. 2.4;

Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 4 RCCLIPACRRNKKFC 19

DB 9 KCCLIGCTKRSKLYC 24

RESULT 23

Q86RB2

ID Q86RB2 PRELIMINARY; PRT; 40 AA.

AC Q86RB2;

DT 01-JUN-2003 (TrEMBLrel. 24, Created)

DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)

DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Alpha-conotoxin G1C precursor (Fragment).

OS Conus geographus (Geography cone).

OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;

OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;

OC Neogastropoda; Conoidea; Conidae; Conus.

NCBI\_TaxID=6491;

[1]

SEQUENCE FROM N.A.

RX MEDLINE=22206623; PubMed=12114524;

RA McIntosh J.M., Dowell C., Watkins M., Garrett J.E., Yoshikami D.,

RA Oliveira B.M.;

"Alpha-Conotoxin G1C from Conus geographus, a Novel Peptide Antagonist

of Nicotinic Acetylcholine Receptors.";

J. Biol. Chem. 277:33610-33615(2002).

EMBL; AF526267; AA033169.1; -

NON\_TER 1

CHAIN 21 36 ALPHA-CONOTOXIN G1C.

SEQUENCE 40 AA; 4246 MW; 1414332030CCS9D CRC64;

Query Match 37.4%; Score 46; DB 5; Length 40;

Best Local Similarity 46.7%; Pred. No. 3.8;

Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 5 CCLIPACRRNKKFC 19

DB 22 CSHFACGNNQHC 36

ULT 24  
4F9

Q854F9 PRELIMINARY; PRT; 125 AA.  
Q854F9; 01-JUN-2003 (TrEMBLrel. 24, Created)  
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
Gp108.  
108.  
Mycobacteriophage Omega.  
Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.  
NCBI\_TaxID=205879;  
[1]  
SEQUENCE FROM N.A.  
MEDLINE=22592660; PubMed=12705866;  
Pedulla M.L., Ford M.E., Houtz J.M., Karthikeyan T., Wadsworth C.,  
Lewis J.A., Jacobs-Sera D., Falbo J., Gross J., Panunzio N.R.,  
Brucker W., Kumar V., Kandasamy J., Keenan L., Bardarov S.,  
Kriakov J., Lawrence J.G., Jacobs W.R. Jr., Hendrix R.W.,  
Hatfull G.F.,  
"Origins of highly mosaic mycobacteriophage genomes.";  
Cell 113:171-182(2003).  
EMBL; AY129338; AAN12749.1; -  
SEQUENCE 125 AA; 14846 MW; C08BBC3D26687306 CRC64;

Query Match 37.4%; Score 46; DB 9; Length 125;  
Best Local Similarity 44.4%; Pred. No. 10;  
Matches 8; Conservative 2; Mismatches 6; Indels 2; Gaps 1;

4 RCCLIPACRRNH--KKFC 19  
2 RTCTIPGCKKHARGFC 19

ULT 25

081217 PRELIMINARY; PRT; 174 AA.  
081217; 01-NOV-1998 (TrEMBLrel. 08, Created)  
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
Trypsin inhibitor.  
Zea mays (Maize).  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
PACCAD clade; Panicoideae; Andropogoneae; Zea.  
NCBI\_TaxID=4577;  
[1]  
SEQUENCE FROM N.A.  
STRAIN=TX5855; TISSUE=Root tip;  
Finkelstein D.B., Drew M.C., Jordan W.J., Wing R.A., Mullet J.E.,  
Morgan P.W.,  
Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.  
EMBL; AF057184; AAC24570.1; -  
PIR; T01649; T01649.  
HSP; P01064; IPI2.  
GO; GO:0005576; C:extracellular; IEA.  
GO; GO:0004867; F:serine protease inhibitor activity; IEA.  
InterPro; IPR000877; Bowman-Birk leg.  
Pfam; PF00228; Bowman-Birk leg; 3.  
ProDom; PD002168; Bowman-Birk leg; 2.  
SMART; SM00269; Bows; 2.  
SEQUENCE 174 AA; 19066 MW; 8F14F058F817046 CRC64;

Query Match 37.4%; Score 46; DB 10; Length 174;  
Best Local Similarity 35.3%; Pred. No. 13;  
Matches 6; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

3 WRCCLIACRRNHKKFC 19  
113 WDCCDFAVCTRDYIPYC 129

RESULT 26

Q96SR6 PRELIMINARY; PRT; 314 AA.  
AC Q96SR6;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Hypothetical protein.  
GN Y37E10B.2  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
OC Rhabditidae; Peloderinae; Caenorhabditis.  
CX NCBI\_TaxID=6239;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Bristol N2;  
RX MEDLINE=99069613; PubMed=9851916;  
RA None;  
RT "Genome sequence of the nematode C. elegans: a platform for  
investigating biology. The C. elegans Sequencing Consortium.";  
RL Science 282:2012-2018(1998).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Bristol N2;  
RX Harmon G., Wohlmann P.;  
RT "The sequence of C. elegans cosmid Y97E10B.";  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Bristol N2;  
RX Waterston R.;  
RT "Direct Submission.";  
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AC024881; AAK71412.2; -  
DR WormPep; Y97E10B.2; CE30329.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.  
DR GO; GO:0007186; P:G-protein coupled receptor protein signaling. .; IEA.  
DR InterPro; IPR000276; GPCR Rhodopsn.  
DR PROSITE; PS0282; G\_PROTEIN\_RECEP\_F1\_2; 1.  
KW Hypothetical protein.  
SQ SEQUENCE 314 AA; 36044 MW; 158694F853AASCA3 CRC64;

Query Match 37.4%; Score 46; DB 5; Length 314;  
Best Local Similarity 53.3%; Pred. No. 22;  
Matches 8; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

Qy 2 NWFCCLIACRRNHK 16  
Db 277 SWSG--IPGCRKLHK 289

RESULT 27

Q69275 PRELIMINARY; PRT; 363 AA.  
AC Q69275;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE US1 protein.  
GN US1.  
OS Equine herpesvirus 4.  
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
OC Alphaherpesvirinae; Varicellovirus.  
CX NCBI\_TaxID=10331;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=405/76;  
RX MEDLINE=93119267; PubMed=8380320;  
RA Nagesha H.S., Studdert M.J., Crabb B.S.;  
RT "Analysis of the nucleotide sequence of five genes at the left end of  
the unique short region of the equine herpesvirus 4 genome.";

Arch. Virol. 128:143-154(1993).  
 EMBL; M89634; AAA46100.1; --  
 PIR; A48338; A48338.  
 SEQUENCE 363 AA; 41068 MW; 3C4096F474C32ED6 CRC64;

Query Match 37.4%; Score 46; DB 12; Length 363;  
 Best Local Similarity 87.5%; Pred. No. 25;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

4 RCCLIPAC 11

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284 RCCLTPAC 291

MULT 28

723

Q8V723 PRELIMINARY; PRT; 401 AA.

Q8V723; 01-MAR-2002 (TrEMBLrel. 20, Created)

01-MAR-2002 (TrEMBLrel. 20, Last sequence update)

01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

Glycoprotein GI.

US7.

Simian herpes B virus (Cercopithecoid herpesvirus 1) (Shbv).

Viruses; dsDNA viruses, no RNA stage; Herpesviridae;

Alphaherpesvirinae; Simplexvirus.

NCBI\_TaxID=10325;

[1]

SEQUENCE FROM N.A.

STRAIN=E2490;

MEDLINE=21635528; PubMed=11773425;

Ohnawa K., Black D.H., Sato H., Eberle R.;

"Sequence and Genetic Arrangement of the Us Region of the Monkey B

Virus (Cercopithecine herpesvirus 1) Genome and Comparison with the Us

Region of Other Primate Herpesviruses.;"

J. Virol. 76:1516-1520(2002).

EMBL; AB074432; BAB83754.1; --

InterPro; IPR002874; Herpes GI.

Pfam; PF01688; Herpes GI; 1.

SEQUENCE 401 AA; 41980 MW; B4D41D21BA3D3AC3 CRC64;

Query Match 37.4%; Score 46; DB 12; Length 401;

Best Local Similarity 53.8%; Pred. No. 27;

Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

5 CCLIPACRRNKKK 17

|||||

308 CCLARRCRRRHR 320

SULT 29

75C2

Q7T5C2 PRELIMINARY; PRT; 401 AA.

Q7T5C2; 01-OCT-2003 (TrEMBLrel. 25, Created)

01-OCT-2003 (TrEMBLrel. 25, Last sequence update)

01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

Virion glycoprotein I.

US7.

Simian herpes B virus (Cercopithecoid herpesvirus 1) (Shbv).

Viruses; dsDNA viruses, no RNA stage; Herpesviridae;

Alphaherpesvirinae; Simplexvirus.

NCBI\_TaxID=10325;

[1]

SEQUENCE FROM N.A.

STRAIN=E2490;

MEDLINE=22628476; PubMed=12743273;

Pereelygina L., Zhu L., Zurkuhlen H., Mills R., Borodovsky M.,

Hilliard J.K.;

"Complete Sequence and Comparative Analysis of the Genome of Herpes B

Virus (Cercopithecine Herpesvirus 1) from a Rhesus Monkey.;"

J. Virol. 77:6167-6177(2003).

EMBL; AF533768; AAP41484.1; --

SQ SEQUENCE 401 AA; 42025 MW; 5DAFECDBB58D357C CRC64;  
 Query Match 37.4%; Score 46; DB 12; Length 401;  
 Best Local Similarity 53.8%; Pred. No. 27;  
 Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 5 CCLIPACRRNKKK 17

|||||

308 CCLARRCRRRHR 320

RESULT 30

Q91YB6

ID Q91YB6 PRELIMINARY; PRT; 1236 AA.

AC Q91YB6;

DT 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE Complement inhibitory factor H.

GN FH.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.

OX NCBI\_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Sprague-Dawley; TISSUE=Liver;

RA Demberg H., Goetze O., Schlaf G.;

RT "Rat complement factor H: molecular cloning, sequencing and expression

in tissues and isolated cells.;"

RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AJ320522; CAC67513.1; --

DR InterPro; IPR000436; Sushi\_SCR\_CCP.

DR InterPro; IPR007087; Znf\_C2H2.

DR Pfam; PF00084; sushi; 20.

DR SMART; SMO0032; CCP; 20.

DR PROSITE; PS00028; ZINC\_FINGER\_C2H2\_1; 1.

SQ SEQUENCE 1236 AA; 140343 MW; 1AC89FFA28232BBF CRC64;

Query Match 37.4%; Score 46; DB 11; Length 1236;

Best Local Similarity 63.6%; Pred. No. 72;

Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 9 PACRRNKKKFC 19

|||||

800 FNCTRNEKRC 910

RESULT 31

Q04923

ID Q04923 PRELIMINARY; PRT; 97 AA.

AC Q04923;

DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Hypothetical protein.

GN YDR220C.

OS Saccharomyces cerevisiae (Baker's yeast).

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.

NCBI\_TaxID=4932;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=AB972;

RA Murphy L., Harris D.;

RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=AB972;

RA Barrell B., Rajandream M.A.;

RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A.



3 WRCLIPACRR 13  
|||  
223 WRGSAFACRR 233

ULT 35  
SH1

Q9XSH1 PRELIMINARY; PRT; 249 AA.  
Q9XSH1;  
01-NOV-1999 (TRENBLrel. 12, Created)  
01-NOV-1999 (TRENBLrel. 12, Last sequence update)  
01-OCT-2003 (TRENBLrel. 25, Last annotation update)  
Membrane-bound folate binding protein.  
Sus scrofa (pig).  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
NCBI\_TaxID=9823;  
[1]  
SEQUENCE FROM N.A.  
TISSUE=Placenta;  
Vallet J.L., Smith T.P.L., Sontegard T., Pearson P.L.,  
Christenson R.K., Klemcke H.G.;  
"Isolation of cDNAs encoding putative secreted and membrane-bound  
folate binding proteins from endometrium of swine."  
Biol. Reprod. 0:0-0(1999).  
EMBL; AF137374; AAD33741.1; -.  
InterPro: IPR004269; Folt\_chemrecept.  
Pfam: PF03024; Folate rec; 1.  
SEQUENCE 249 AA; 28755 MW; 17FAAF2001D6B420 CRC64;  
Query Match 36.6%; Score 45; DB 6; Length 249;  
Best Local Similarity 50.0%; Pred. No. 26;  
Matches 8; Conservative 3; Mismatches 3; Indels 2; Gaps 1;  
1 FNRCC-LIPACRN 14  
||| : |||:  
76 FNRHCGNKPCKRH 91

arch completed: February 18, 2004, 06:09:40  
> time : 83 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

protein - protein search, using sw model

on: February 18, 2004, 06:03:18 ; Search time 95 seconds

(without alignments)  
56.510 Million cell updates/sec

le: US-09-806-376-1

fect score: 123

uence: 1 FNRCCCLIPACRNNKKFC 19

ring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

ched: 1586107 seqs, 282547505 residues

al number of hits satisfying chosen parameters: 1586107

imum DB seq length: 0

imum DB seq length: 2000000000

t-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

abase : A Geneseq 29Jan04:\*

1: Geneseqp1980s:\*

2: Geneseqp1990s:\*

3: Geneseqp2000s:\*

4: Geneseqp2001s:\*

5: Geneseqp2002s:\*

6: Geneseqp2003as:\*

7: Geneseqp2003bs:\*

8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ult No.	Score	Query Match	Length	DB ID	Description
1	123	100.0	19	3	AAY92227 Rho-Conto
2	95	77.2	15	3	AAY92228 Truncated
3	56.5	45.9	40	3	AAB21635 Cone snai
4	55	44.7	24	3	AAB21612 Cone snai
5	55	44.7	38	3	AAB21610 Cone snai
6	54.5	44.3	38	3	AAB21637 Cone snai
7	52	42.3	61	3	AAB21450 Cone snai
8	52	42.3	62	3	AAB21440 Cone snai
9	52	42.3	62	3	AAB21616 Cone snai
10	52	42.3	64	3	AAB21452 Cone snai
11	51	41.5	60	3	AAB21581 Cone snai
12	51	41.5	221	4	ABG04153 Novel hum
13	50	40.7	18	2	AAR75280 A-lineage
14	50	40.7	18	2	AAW12742 A-lineage
15	50	40.7	37	3	AAB21625 Cone snai
16	50	40.7	40	3	AAB21622 Cone snai
17	50	40.7	65	3	AAB21443 Cone snai
18	50	40.7	76	5	ABB88269 C radiatu
19	49	39.8	16	2	AAW75275 A-lineage
20	49	39.8	16	2	AAW24882 Predatory
21	49	39.8	16	2	AAW12737 A-lineage
22	49	39.8	16	6	ABP60018 Alpha-con
23	49	39.8	17	5	ABG99820 Conus sp
24	49	39.8	18	3	AAB21436 Cone snai
25	49	39.8	25	3	AAB21617 Cone snai

26	49	39.8	60	5	ABG99639 Conus sp
27	49	39.8	61	3	AAB21431 Cone snai
28	49	39.8	61	3	AAB21433 Cone snai
29	49	39.8	747	4	ABG11569 Novel hum
30	48	39.0	16	2	AY24163 Alpha-Con
31	48	39.0	18	2	AAW24887 Predatory
32	48	39.0	18	3	AAW87522 Mature co
33	48	39.0	18	3	AAB21523 Cone snai
34	48	39.0	38	3	AAB21634 Cone snai
35	48	39.0	39	3	AAB21586 Cone snai
36	48	39.0	40	3	AAB21591 Cone snai
37	48	39.0	40	3	AAB21623 Cone snai
38	48	39.0	41	3	AAB21578 Cone snai
39	48	39.0	41	3	AAB21598 Cone snai
40	48	39.0	60	3	AAB21462 Cone snai
41	48	39.0	61	3	AAB21432 Cone snai
42	48	39.0	65	3	AAB38378 Human sec
43	48	39.0	66	3	AY87523 Conotoxin
44	48	39.0	76	4	AAU86446 Novel hum
45	48	39.0	76	4	AD859780 Connectiv
46	48	39.0	150	4	AAE03779 Human gen
47	48	39.0	150	4	AA885556 Human sec
48	48	39.0	150	4	AA885536 Human sec
49	48	39.0	150	5	ABG76602 Human sec
50	48	39.0	150	5	ABG76582 Human sec

ALIGNMENTS

RESULT 1

RAY92227  
ID AAY92227 standard; peptide; 19 AA.

XX AC RAY92227;

DT 10-AUG-2000 (first entry)

XX Rho-conotoxin peptide, rho-TIA.

XX Rho-conotoxin; alpha-1-adrenoreceptor; antagonist; hypotensive; cardiast;  
analgesic; antiarrhythmic; cytostatic; nootropic; antinflammatory.

XX Conus tulipa.

XX Key Location/Qualifiers

FT Disulfide-bond 5 /note= "involved in disulphide bond"

FT Disulfide-bond 6 /note= "involved in disulphide bond"

FT Disulfide-bond 11 /note= "involved in disulphide bond"

FT Disulfide-bond 19 /note= "involved in disulphide bond"

XX WO200020443-A1.

XX 13-APR-2000.

XX 01-OCT-1999; 99WO-AU000843.

XX 02-OCT-1998; 98AU-00006273.

XX (UYQU ) UNIV QUEENSLAND.

XX Lewis RJ, Alewood PF, Sharpe IA;

XX WPI; 2000-303737/26.

Isolated rho-conotoxin peptide used for the treatment of urinary or  
cardiovascular conditions or diseases, mood disorders or for control of  
pain or inflammation comprises selective alpha1-adrenoceptor antagonist  
activity.

Claim 2; Page 31; 47pp; English.

The rho-conotoxin peptide, rho-TIA, is isolated from the venom duct of the fish hunting cone snail *Conus tulipa*. It contains two disulphide bonds. The rho-conotoxin peptide has selective alpha-1-adrenoceptor antagonist activity. It can be used in a receptor binding assay to test the activity of a molecule as an antagonist of alpha-1-adrenoceptor activity. Rho-TIA is labeled, e.g. with radioactive isotope and used to identify molecules which act at the same site. Antibodies to rho-TIA are useful as therapeutic and diagnostic agents. Rho-conotoxin can be used for the treatment of or prophylaxis of a urinary system disease, e.g. prostatic hyperplasia, cardiovascular disease, e.g. arrhythmia, hypertension or coronary heart failure, a mood disorder, e.g. craving (e.g. smoking craving) and pain, e.g. chronic pain, neuropathic pain or inflammatory pain (all claimed).

Sequence 19 AA;

Query Match 100.0%; Score 123; DB 3; Length 19;  
Best Local Similarity 100.0%; Pred. NO. 4.7e-09;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 FNRCCCLIPACRRNHKKFC 19  
|||||  
1 FNRCCCLIPACRRNHKKFC 19

ULT 2  
92228

AA92228 standard; peptide; 15 AA.

AA922228;

10-AUG-2000 (first entry)

Truncated, inactive rho-conotoxin peptide derivative.

Rho-conotoxin; alpha-1-adrenoceptor; antagonist; hypotensive; cardiant; analgesic; antiarrhythmic; cyrostatic; nootropic; antiinflammatory.

*Conus tulipa*.  
Synthetic.

Key	Location/Qualifiers
Disulfide-bond 5	/note= "involved in disulphide bond"
Disulfide-bond 6	/note= "involved in disulphide bond"
Disulfide-bond 11	/note= "involved in disulphide bond"
Disulfide-bond 19	/note= "involved in disulphide bond"

WO200020443-A1.

13-APR-2000.

01-OCT-1999; 99WO-AU000843.

02-OCT-1998; 98AU-00006273.

(UYQU ) UNIV QUEENSLAND.

Lewis RJ, Alewood PF, Sharpe IA;

WPI; 2000-303737/26.

Isolated rho-conotoxin peptide used for the treatment of urinary or cardiovascular conditions or diseases, mood disorders or for control of pain or inflammation comprises selective alpha-1-adrenoceptor antagonist activity.

PS Disclosure; Page 3; 47pp; English.

XX The rho-conotoxin peptide, rho-TIA (see AAY92227), is isolated from the venom duct of the fish hunting cone snail *Conus tulipa*. It contains two disulphide bonds. The rho-conotoxin peptide has selective alpha-1-adrenoceptor antagonist activity. It can be used in a receptor binding assay to test the activity of a molecule as an antagonist of alpha-1-adrenoceptor activity. Rho-TIA is labeled, e.g. with radioactive isotope and used to identify molecules which act at the same site. Antibodies to rho-TIA are useful as therapeutic and diagnostic agents. Rho-conotoxin can be used for the treatment of or prophylaxis of a urinary system disease, e.g. prostatic hyperplasia, cardiovascular disease, e.g. arrhythmia, hypertension or coronary heart failure, a mood disorder, e.g. craving (e.g. smoking craving) and pain, e.g. chronic pain, neuropathic pain or inflammatory pain (all claimed).

SQ Sequence 15 AA;

Query Match 77.2%; Score 95; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. NO. 1.5e-05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CCLIPACRRNHKKFC 19  
|||||  
Db 1 CCLIPACRRNHKKFC 15

RESULT 3

AAAB21635  
ID AAB21635 standard; peptide; 40 AA.

XX AAB21635;

XX 19-JAN-2001 (first entry)

XX Cone snail alpha-conotoxin SEQ ID NO: 398.

XX Cone snail; alpha-conotoxin; venom; disulphide bond; mood disorder;  
KW neuronal nicotinic acetylcholine receptor; cardiovascular disorder;  
KW gastric motility disorder; urinary incontinence; nicotine addiction;  
KW small cell lung carcinoma.

XX *Conus tulipa*.

XX WO200044776-A1.

XX 03-AUG-2000.

XX 28-JAN-2000; 2000WO-US001979.

XX 29-JAN-1999; 99US-0118381P.

XX (UTAH ) UNIV UTAH RES FOUND.

XX (COGN-) COGNETIX INC.

XX Watkins M, Olivera BM, Hillyard DR, McIntosh JM, Jones RM;

XX WPI; 2000-505965/45.

XX N-ESDB; AAA89531.

XX alpha-conotoxin polypeptides derived from the venom of cone snails useful e.g. as neuromuscular blocking agents for use in surgery and for treating unipolar depression.

XX Claim 39; Page 66; 229pp; English.

XX The present invention relates to a number of alpha-conotoxin peptides and their coding sequences from a number of different species of cone snail. These peptides are found in minute quantities in the venom of the snails, and are targeted at the neuronal nicotinic acetylcholine receptors of the nervous system. They usually contain two disulphide bonds, which give them defined conformations, a rarity in molecules this small. The alpha-conotoxins can be used as neuromuscular blocking agents in surgery, and

for treating disorders regulated at the neuronal nicotinic acetylcholine receptors, including cardiovascular disorders, gastric motility disorders, urinary incontinence, nicotine addiction, mood disorders such as bipolar disorder, unipolar depression, dysthymia and seasonal affective disorder, and small cell lung carcinoma

Sequence 40 AA;

Query Match 45.9%; Score 56.5; DB 3; Length 40;  
Best Local Similarity 55.6%; Pred. No. 3;  
Matches 10; Conservative 1; Mismatches 6; Indels 1; Gaps 1;

3 WR-CCLPACRRNHKKFC 19  
||| ||| ||| :  
19 WEGCCSNPACLNVNHRFC 35

ULT 4  
321612

AAB21612 standard; peptide; 24 AA.

AAB21612;

19-JAN-2001 (first entry)

Cone snail alpha-conotoxin SEQ ID NO: 352.

Cone snail; alpha-conotoxin; venom; disulphide bond; mood disorder;  
neuronal nicotinic acetylcholine receptor; cardiovascular disorder;  
gastric motility disorder; urinary incontinence; nicotine addiction;  
small cell lung carcinoma.

Conus obscurus.

WO200044776-A1.

03-AUG-2000.

28-JAN-2000; 2000WO-US001979.

29-JAN-1999; 99US-0118381P.

(UTAH) UNIV UTAH RES FOUND.  
(COGN-) COGNETIX INC.

Watkins M, Olivera BM, Hillyard DR, McIntosh JM, Jones RM;

WPI; 2000-505965/45.  
N-PSDB; AAA89508.

alpha-conotoxin polypeptides derived from the venom of cone snails useful  
e.g. as neuromuscular blocking agents for use in surgery and for treating  
unipolar depression.

Claim 39; Page 60; 229pp; English.

The present invention relates to a number of alpha-conotoxin peptides and  
their coding sequences from a number of different species of cone snail.  
These peptides are found in minute quantities in the venom of the snails,  
and are targeted at the neuronal nicotinic acetylcholine receptors of the  
nervous system. They usually contain two disulphide bonds, which give  
them defined conformations, a rarity in molecules this small. The alpha-  
conotoxins can be used as neuromuscular blocking agents in surgery, and  
for treating disorders regulated at the neuronal nicotinic acetylcholine  
receptors, including cardiovascular disorders, gastric motility  
disorders, urinary incontinence, nicotine addiction, mood disorders such  
as bipolar disorder, unipolar depression, dysthymia and seasonal  
affective disorder, and small cell lung carcinoma

Sequence 24 AA;

Query Match 44.7%; Score 55; DB 3; Length 24;  
Best Local Similarity 53.3%; Pred. No. 3.1;

Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
Qy 5 CCLIPACRRNHKKFC 19  
||| ||| ||| :  
Db 6 CSHPVCRFNPVKYC 20

RESULT 5

AAB21610

ID AAB21610 standard; peptide; 38 AA.

XX

AC AAB21610;

XX

DT 19-JAN-2001 (first entry)

XX

DE Cone snail alpha-conotoxin SEQ ID NO: 348.

XX

Cone snail; alpha-conotoxin; venom; disulphide bond; mood disorder;  
neuronal nicotinic acetylcholine receptor; cardiovascular disorder;  
gastric motility disorder; urinary incontinence; nicotine addiction;  
small cell lung carcinoma.

XX

OS Conus musicus.

XX

PN WO200044776-A1.

XX

PD 03-AUG-2000.

XX

PF 28-JAN-2000; 2000WO-US001979.

XX

PR 29-JAN-1999; 99US-0118381P.

XX

PA (UTAH) UNIV UTAH RES FOUND.

XX

PA (COGN-) COGNETIX INC.

XX

PI Watkins M, Olivera BM, Hillyard DR, McIntosh JM, Jones RM;

XX

DR WPI; 2000-505965/45.

XX

DR N-PSDB; AAA89506.

alpha-conotoxin polypeptides derived from the venom of cone snails useful  
e.g. as neuromuscular blocking agents for use in surgery and for treating  
unipolar depression.

Claim 39; Page 59; 229pp; English.

The present invention relates to a number of alpha-conotoxin peptides and  
their coding sequences from a number of different species of cone snail.  
These peptides are found in minute quantities in the venom of the snails,  
and are targeted at the neuronal nicotinic acetylcholine receptors of the  
nervous system. They usually contain two disulphide bonds, which give  
them defined conformations, a rarity in molecules this small. The alpha-  
conotoxins can be used as neuromuscular blocking agents in surgery, and  
for treating disorders regulated at the neuronal nicotinic acetylcholine  
receptors, including cardiovascular disorders, gastric motility  
disorders, urinary incontinence, nicotine addiction, mood disorders such  
as bipolar disorder, unipolar depression, dysthymia and seasonal  
affective disorder, and small cell lung carcinoma

XX Sequence 38 AA;

Query Match 44.7%; Score 55; DB 3; Length 38;

Best Local Similarity 43.8%; Pred. No. 4.5;

Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 4 RCLIPACRRNHKKFC 19

||| ||| ||| :  
Db 19 KCCINDACRSKHPQYC 34

RESULT 6

AAB21637

ID AAB21637 standard; peptide; 38 AA.

Cone snail; alpha-conotoxin; venom; disulphide bond; mood disorder; neuronal nicotinic acetylcholine receptor; cardiovascular disorder; gastric motility disorder; urinary incontinence; nicotine addiction;



29-JAN-1999; 99US-0118381P.

(UTAH ) UNIV UTAH RES FOUND.  
(COGN-) COGNETIX INC.

Watkins M, Olivera BM, Hillyard DR, McIntosh JM, Jones RM;

WPI; 2000-505965/45.  
N-PSDB; AAA89415.

alpha-conotoxin polypeptides derived from the venom of cone snails useful  
e.g. as neuromuscular blocking agents for use in surgery and for treating  
unipolar depression.

Claim 39; Page 35-36; 229pp; English.

The present invention relates to a number of alpha-conotoxin peptides and  
their coding sequences from a number of different species of cone snail.  
These peptides are found in minute quantities in the venom of the snails,  
and are targeted at the neuronal nicotinic acetylcholine receptors of the  
nervous system. They usually contain two disulphide bonds, which give  
them defined conformations, a rarity in molecules this small. The alpha-  
conotoxins can be used as neuromuscular blocking agents in surgery, and  
for treating disorders regulated at the neuronal nicotinic acetylcholine  
receptors, including cardiovascular disorders, gastric motility  
disorders, urinary incontinence, nicotine addiction, mood disorders such  
as bipolar disorder, unipolar depression, dysthymia and seasonal  
affective disorder, and small cell lung carcinoma

Sequence 62 AA;

Query Match 42.3%; Score 52; DB 3; Length 62;  
est Local Similarity 53.3%; Pred. No. 16;  
atches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

5 CCLIPACRRNKKFC 19  
||| ||| | : ||  
44 CCHPACSGNNPFC 58

UIT 9

21616  
AAB21616 standard; peptide; 62 AA.

AAB21616;

19-JAN-2001 (first entry)

Cone snail alpha-conotoxin SEQ ID NO: 360.

Cone snail; alpha-conotoxin; venom; disulphide bond; mood disorder;  
neuronal nicotinic acetylcholine receptor; cardiovascular disorder;  
gastric motility disorder; urinary incontinence; nicotine addiction;  
small cell lung carcinoma.

Conus obscurus.

WO200044776-A1.

03-AUG-2000.

28-JAN-2000; 2000WO-US001979.

29-JAN-1999; 99US-0118381P.

(UTAH ) UNIV UTAH RES FOUND.  
(COGN-) COGNETIX INC.

Watkins M, Olivera BM, Hillyard DR, McIntosh JM, Jones RM;

WPI; 2000-505965/45.  
N-PSDB; AAA89512.

PT alpha-conotoxin polypeptides derived from the venom of cone snails useful  
PT e.g. as neuromuscular blocking agents for use in surgery and for treating  
PT unipolar depression.

XX Claim 39; Page 61; 229pp; English.

XX The present invention relates to a number of alpha-conotoxin peptides and  
CC their coding sequences from a number of different species of cone snail.  
CC These peptides are found in minute quantities in the venom of the snails,  
CC and are targeted at the neuronal nicotinic acetylcholine receptors of the  
CC nervous system. They usually contain two disulphide bonds, which give  
CC them defined conformations, a rarity in molecules this small. The alpha-  
CC conotoxins can be used as neuromuscular blocking agents in surgery, and  
CC for treating disorders regulated at the neuronal nicotinic acetylcholine  
CC receptors, including cardiovascular disorders, gastric motility  
CC disorders, urinary incontinence, nicotine addiction, mood disorders such  
CC as bipolar disorder, unipolar depression, dysthymia and seasonal  
CC affective disorder, and small cell lung carcinoma

XX Sequence 62 AA;

Query Match 42.3%; Score 52; DB 3; Length 62;  
Best Local Similarity 46.7%; Pred. No. 16;  
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 5 CCLIPACRRNKKFC 19

Db 44 CCHPACSGNNREYC 58

RESULT 10

AAB21452

ID AAB21452 standard; protein; 64 AA.

XX AAB21452;

19-JAN-2001 (first entry)

Cone snail alpha-conotoxin SEQ ID NO: 111.

Cone snail; alpha-conotoxin; venom; disulphide bond; mood disorder;  
neuronal nicotinic acetylcholine receptor; cardiovascular disorder;  
gastric motility disorder; urinary incontinence; nicotine addiction;  
small cell lung carcinoma.

OS Conus betulinus.

XX WO200044776-A1.

XX 03-AUG-2000.

XX 28-JAN-2000; 2000WO-US001979.

XX 29-JAN-1999; 99US-0118381P.

XX (UTAH ) UNIV UTAH RES FOUND.

XX (COGN-) COGNETIX INC.

XX Watkins M, Olivera BM, Hillyard DR, McIntosh JM, Jones RM;

XX WPI; 2000-505965/45.

XX N-PSDB; AAA89427.

PT alpha-conotoxin polypeptides derived from the venom of cone snails useful  
PT e.g. as neuromuscular blocking agents for use in surgery and for treating  
PT unipolar depression.

XX Claim 39; Page 39; 229pp; English.

XX The present invention relates to a number of alpha-conotoxin peptides and  
CC their coding sequences from a number of different species of cone snail.  
CC These peptides are found in minute quantities in the venom of the snails,  
CC and are targeted at the neuronal nicotinic acetylcholine receptors of the

nervous system. They usually contain two disulphide bonds, which give them defined conformations, a rarity in molecules this small. The alpha-conotoxins can be used as neuromuscular blocking agents in surgery, and for treating disorders regulated at the neuronal nicotinic acetylcholine receptors, including cardiovascular disorders, gastric motility disorders, urinary incontinence, nicotine addiction, mood disorders such as bipolar disorder, unipolar depression, dysthymia and seasonal affective disorder, and small cell lung carcinoma

Sequence 64 AA;

Query Match 42.3%; Score 52; DB 3; Length 64;  
Best Local Similarity 53.3%; Pred. No. 17;  
Matches 8; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

5 CCLIPACRRNHKKFC 19  
||| ||| : :  
46 CCSHPACSVNHPCLC 60

MULT 11  
121581

AAB21581 standard; peptide; 60 AA.

AAB21581;

19-JAN-2001 (first entry)

Cone snail alpha-conotoxin SEQ ID NO: 290.

Cone snail; alpha-conotoxin; venom; disulphide bond; mood disorder;  
neuronal nicotinic acetylcholine receptor; cardiovascular disorder;  
gastric motility disorder; urinary incontinence; nicotine addiction;  
small cell lung carcinoma.

Conus ammiralis.

WO200044776-A1.

03-AUG-2000.

28-JAN-2000; 2000WO-US001979.

29-JAN-1999; 99US-011838-P.

(UTAH) UNIV UTAH RES FOUND.  
(COGN-) COGNEX INC.

Watkins M, Olivera BM, Hillyard DR, McIntosh JM, Jones RM;

WPI; 2000-505965/45.  
N-PSDB; AAA89477.

alpha-conotoxin polypeptides derived from the venom of cone snails useful  
e.g. as neuromuscular blocking agents for use in surgery and for treating  
unipolar depression.

Claim 39; Page 52; 229pp; English.

The present invention relates to a number of alpha-conotoxin peptides and  
their coding sequences from a number of different species of cone snail.  
These peptides are found in minute quantities in the venom of the snails,  
and are targeted at the neuronal nicotinic acetylcholine receptors of the  
nervous system. They usually contain two disulphide bonds, which give  
them defined conformations, a rarity in molecules this small. The alpha-  
conotoxins can be used as neuromuscular blocking agents in surgery, and  
for treating disorders regulated at the neuronal nicotinic acetylcholine  
receptors, including cardiovascular disorders, gastric motility  
disorders, urinary incontinence, nicotine addiction, mood disorders such  
as bipolar disorder, unipolar depression, dysthymia and seasonal  
affective disorder, and small cell lung carcinoma

Sequence 60 AA;

Query Match 41.5%; Score 51; DB 4; Length 221;

Query Match 41.5%; Score 51; DB 3; Length 60;  
Best Local Similarity 46.7%; Pred. No. 22;  
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 5 CCLIPACRRNHKKFC 19  
||| ||| : :  
DB 45 CCSYPACNLDHPELC 59

RESULT 12

ABG04153

ID ASS04153 standard; protein; 221 AA.

AC ABG04153;

DT 13-FEB-2002 (first entry)

DE Novel human diagnostic protein #4144.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;  
KW food supplement; medical imaging; diagnostic; genetic disorder.

XX Homo sapiens.

XX WO200175067-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US008631.

XX 31-MAR-2000; 2000US-00540217.

PR 23-AUG-2000; 2000US-00649167.

XX (HYSE-) HYSEQ INC.

PA

XX Drmanac RT, Liu C, Tang YT;

XX WPI; 2001-639362/73.

DR N-PSDB; AAS68340.

XX New isolated polynucleotide and encoded polypeptides, useful in  
PT diagnostics, forensics, gene mapping, identification of mutations  
PT responsible for genetic disorders or other traits and to assess  
PT biodiversity.

XX Claim 20; SEQ ID NO 34512; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II)  
CC sequences. (I) is useful as hybridisation probes, polymerase chain  
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping.  
CC and in recombinant production of (II). The polynucleotides are also used  
CC in diagnostics as expressed sequence tags for identifying expressed  
CC genes. (I) is useful in gene therapy techniques to restore normal  
CC activity of (II) or to treat disease states involving (II). (II) is  
CC useful for generating antibodies against it, detecting or quantitating a  
CC polypeptide in tissue, as molecular weight markers and as a food  
CC supplement. (II) and its binding partners are useful in medical imaging  
CC of sites expressing (II). (I) and (II) are useful for treating disorders  
CC involving aberrant protein expression or biological activity. The  
CC polypeptide and polynucleotide sequences have applications in  
CC diagnostics, forensics, gene mapping, identification of mutations  
CC and to produce other types of data and products dependent on DNA and  
CC amino acid sequences. ABG0010-ABG30377 represent novel human diagnostic  
CC patent did not appear in the printed specification. Note: The sequence data for this  
CC electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 221 AA;

Query Match 41.5%; Score 51; DB 4; Length 221;

est Local Similarity 50.0%; Pred. No. 64;  
atches 8; Conservative 4; Mismatches 2; Indels 2; Gaps 1;  
1 FNNRCC--LIPACRRN 14  
81 FNNHCGEMVPACKRH 96

ULT 13  
75280  
AAR75280 standard; peptide; 18 AA.

AAR75280;

22-DEC-1995 (first entry)

A-lineage conotoxin SL-1 peptide.

Alpha conotoxin; neuromuscular; synapse; signal transmission.

Conus sulcatus.

Key Location/Qualifiers

Misc-difference 7 /label= Pro or OTHER /note= "Hydroxyproline"

Misc-difference 14 /label= Pro or OTHER /note= "Hydroxyproline"

Modified-site 15 /note= "Glu, can form a peptide bond via either the alpha or gamma carboxyl group"

Modified-site 18 /note= "preferably amidated"

W09511256-A1.

27-APR-1995.

19-OCT-1994; 94WO-US011927.

19-OCT-1993; 93US-00137800.

(UTAH ) UNIV UTAH RES FOUND.

Olivera BM, Cruz LJ, Hillyard DR, McIntosh JM, Santos AD;

WPI; 1995-170189/22.

New A-lineage conotoxin peptide(s) - which inhibit synaptic transmission at the neuromuscular junction or are active against potassium or sodium channels.

Claim 1; Page 44; 66pp; English.

The kappa-conotoxin, alpha conotoxin and alpha-like conotoxin peptides all belong to a group of peptides known as the A-lineage conotoxin peptides. The A lineage conotoxin peptides have a wide variety of pharmacological uses. The A-lineage conotoxin peptides claimed (AAR75264-R75293) are useful for the inhibition of synaptic transmission at neuromuscular junctions by blocking nicotinic acetyl choline receptors and they also have activity against voltage-gated Na and K channels

Sequence 18 AA;

Query Match 40.7%; Score 50; DB 2; Length 18;  
Best Local Similarity 46.7%; Pred. No. 11;  
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

5 CCLIPACRRNHKKFC 19

3 CCSFPACKRYPEMC 17

RESULT 14  
AAW12742  
ID AAW12742 standard; peptide; 18 AA.

AC AAW12742;

25-MAR-2003 (revised)

16-APR-1997 (first entry)

A-lineage conotoxin peptide SL-1.

Polymerase chain reaction; PCR; primer; amplify; conotoxin; Conus; inhibitor; synaptic transmission; neuromuscular junction; sodium channel; nicotinic acetylcholine receptor; potassium channel; muscle relaxant; myasthenia gravis; small cell lung cancer; therapy.

Conus sulcatus.

Key Location/Qualifiers

Modified-site 7 /note= "optionally hydroxylated"

Modified-site 14 /note= "optionally hydroxylated"

Modified-site 15 /note= "optionally gamma-carboxylated"

Modified-site 18 /note= "amidated"

US5589340-A.

31-DEC-1996.

07-JUN-1995; 95US-00477383.

29-JUN-1993; 93US-00084848.

19-OCT-1993; 93US-00137800.

(UTAH ) UNIV UTAH RES FOUND.

Santos AD, Hillyard DR, McIntosh JM, Olivera BM, Cruz LJ;

WPI; 1997-076840/07.

Identifying nucleic acid encoding A-lineage conotoxin peptide(s) by amplification - uses primers corresponding to conserved regions in the signal sequence and 3'-untranslated regions, useful e.g. in treatment of small cell lung cancer.

Disclosure; Col 5; 36pp; English.

AAW12726-W12769 represent conotoxin peptides. This sequence represents the A-lineage conotoxin SL-1 peptide isolated from Conus sulcatus. These sequences are identified using the method of the invention. The method of the invention is for identifying DNA encoding A-lineage conotoxin peptides by subjecting Conus nucleic acid to amplification with primer sequences (see AAR59714 and AAR59715). The primers are specific for the signal sequence and 3'-untranslated (3'UTR) regions of the conotoxin gene, which are highly homologous between conotoxins, and are therefore suitable sites for detection. A-lineage conotoxins include alpha-conotoxins, and kappa-conotoxins. Alpha-conotoxins are powerful inhibitors of synaptic transmission at the neuromuscular junction, and are usually nicotinic acetylcholine receptor blockers. Kappa-conotoxins act on the voltage sensitive sodium and potassium channels. The conotoxins identified can be used as muscle relaxants in the diagnosis of myasthenia gravis, and for the treatment or diagnosis of small cell lung cancer. For the treatment of small cell lung cancer, the conotoxin peptides act by binding to the nicotinic receptors, and thereby blocking the nicotine/cytosine stimulated release of the mitogen 5-hydroxytryptamine. (Updated on 25-MAR-2003 to correct PF field.)

Sequence 18 AA;

Query Match 40.7%; Score 50; DB 2; Length 18;  
 est Local Similarity 46.7%; Pred. No. 11;  
 atches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

5 CCLIPACRRNHKKFC 19  
 ||||| : :  
 3 CCSPACKRYRPMC 17

ULT 15

21625

AAB21625 standard; peptide; 37 AA.

AAB21625;

19-JAN-2001 (first entry)

Cone snail alpha-conotoxin SEQ ID NO: 378.

Cone snail; alpha-conotoxin; venom; disulphide bond; mood disorder;  
 neuronal nicotinic acetylcholine receptor; cardiovascular disorder;  
 gastric motility disorder; urinary incontinence; nicotine addiction;  
 small cell lung carcinoma.

Conus purpurascens.

WC200044776-A1.

03-AUG-2000.

28-JAN-2000; 2000WC-US001979.

29-JAN-1999; 99US-0118381P.

(UTAH ) UNIV UTAH RES FOUND.  
 (COGN-) COGNETIX INC.

Watkins M, Olivera BM, Hillyard DR, McIntosh JM, Jones RM;

WPI; 2000-505965/45.

N-PSDB; AAA89521.

alpha-conotoxin polypeptides derived from the venom of cone snails useful  
 e.g. as neuromuscular blocking agents for use in surgery and for treating  
 unipolar depression.

Claim 39; Page 63; 229pp; English.

The present invention relates to a number of alpha-conotoxin peptides and  
 their coding sequences from a number of different species of cone snail.  
 These peptides are found in minute quantities in the venom of the snails,  
 and are targeted at the neuronal nicotinic acetylcholine receptors of the  
 nervous system. They usually contain two disulphide bonds, which give  
 them defined conformations, a rarity in molecules this small. The alpha-  
 conotoxins can be used as neuromuscular blocking agents in surgery, and  
 for treating disorders regulated at the neuronal nicotinic acetylcholine  
 receptors, including cardiovascular disorders, gastric motility  
 disorders, urinary incontinence, nicotine addiction, mood disorders such  
 as bipolar disorder, unipolar depression, dysthymia and seasonal  
 affective disorder, and small cell lung carcinoma

Sequence 37 AA;

Query Match 40.7%; Score 50; DB 3; Length 37;  
 est Local Similarity 53.3%; Pred. No. 19;  
 Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

5 CCLIPACRRNHKKFC 19  
 ||||| : :  
 19 CCTNPACLVNHRFC 33

SULT 16

AAB21622

ID AAB21622 standard; peptide; 40 AA.

XX AAB21622;

DT 19-JAN-2001 (first entry)

XX Cone snail alpha-conotoxin SEQ ID NO: 372.

XX Cone snail; alpha-conotoxin; venom; disulphide bond; mood disorder;  
 XX neuronal nicotinic acetylcholine receptor; cardiovascular disorder;  
 XX gastric motility disorder; urinary incontinence; nicotine addiction;  
 XX small cell lung carcinoma.

XX Conus purpurascens.

XX WO200044776-A1.

XX 03-AUG-2000.

XX 28-JAN-2000; 2000WC-US001979.

XX 29-JAN-1999; 99US-0118381P.

XX (UTAH ) UNIV UTAH RES FOUND.  
 XX (COGN-) COGNETIX INC.

XX Watkins M, Olivera BM, Hillyard DR, McIntosh JM, Jones RM;

XX WPI; 2000-505965/45.

XX N-PSDB; AAA89518.

XX alpha-conotoxin polypeptides derived from the venom of cone snails useful  
 e.g. as neuromuscular blocking agents for use in surgery and for treating  
 unipolar depression.

XX Claim 39; Page 62; 229pp; English.

XX The present invention relates to a number of alpha-conotoxin peptides and  
 their coding sequences from a number of different species of cone snail.  
 XX These peptides are found in minute quantities in the venom of the snails,  
 XX and are targeted at the neuronal nicotinic acetylcholine receptors of the  
 XX nervous system. They usually contain two disulphide bonds, which give  
 XX them defined conformations, a rarity in molecules this small. The alpha-  
 XX conotoxins can be used as neuromuscular blocking agents in surgery, and  
 XX for treating disorders regulated at the neuronal nicotinic acetylcholine  
 XX receptors, including cardiovascular disorders, gastric motility  
 XX disorders, urinary incontinence, nicotine addiction, mood disorders such  
 XX as bipolar disorder, unipolar depression, dysthymia and seasonal  
 XX affective disorder, and small cell lung carcinoma

XX Sequence 40 AA;

Query Match 40.7%; Score 50; DB 3; Length 40;  
 Best Local Similarity 53.3%; Pred. No. 21;  
 Matches 8; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 5 CCLIPACRRNHKKFC 19

DB 22 CCNPACTLVNHRFC 36

RESULT 17

AAB21443

ID AAB21443 standard; protein; 65 AA.

XX AAB21443;

DT 19-JAN-2001 (first entry)

XX Cone snail alpha-conotoxin SEQ ID NO: 93.

XX Cone snail; alpha-conotoxin; venom; disulphide bond; mood disorder;



neuronal nicotinic acetylcholine receptor; cardiovascular disorder;  
gastric motility disorder; urinary incontinence; nicotine addiction;  
small cell lung carcinoma.

Conus sulcatus.

WC2000044776-A1.

03-AUG-2000.

28-JAN-2000; 2000WO-US001979.

29-JAN-1999; 99US-011838P.

(UTAH ) UNIV UTAH RES FOUND.  
(COGN-) COGNETIX INC.

Watkins M, Olivera BM, Hillyard DR, McIntosh JM, Jones RM;

WPI; 2000-505965/45.  
N-PSDB; AAA89418.

alpha-conotoxin polypeptides derived from the venom of cone snails useful  
e.g. as neuromuscular blocking agents for use in surgery and for treating  
unipolar depression.

Claim 39; Page 36-37; 229pp; English.

The present invention relates to a number of alpha-conotoxin peptides and  
their coding sequences from a number of different species of cone snail.  
These peptides are found in minute quantities in the venom of cone snails,  
and are targeted at the neuronal nicotinic acetylcholine receptors of the  
nervous system. They usually contain two disulphide bonds, which give  
them defined conformations, a rarity in molecules this small. The alpha-  
conotoxins can be used as neuromuscular blocking agents in surgery, and  
for treating disorders regulated at the neuronal nicotinic acetylcholine  
receptors, including cardiovascular disorders, gastric motility  
disorders, urinary incontinence, nicotine addiction, mood disorders such  
as bipolar disorder, unipolar depression, dysthymia and seasonal  
affective disorder, and small cell lung carcinoma

Sequence 65 AA;

Query Match 40.7%; Score 50; DB 3; Length 65;  
Best Local Similarity 46.7%; Pred. No. 31;  
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

5 CCLIPACRHHKFC 19

47 CCSFPACRYRPMC 61

SULT 18

B88269

ABB88269 standard; protein; 76 AA.

ABB88269;

24-MAY-2002 (first entry)

C radiatus mu-conopeptide R3-1 propeptide.

Mu-conopeptide; snail; venom; voltage-gated sodium channel; analgesic;  
anaesthetic; neuromuscular blocking agent; neuroprotective; pain;  
cerebroprotective; anticonvulsant; antiaging; antidiabetic;  
cardiovascular; vasotropic; cardiac; tranquilizer; antimigraine;  
neurodegenerative disease; neuromuscular disorder.

Conus radiatus.

WC200207678-A2.

31-JAN-2002.

XX 23-JUL-2001; 2001WO-US023125.

XX 21-JUL-2000; 2000US-0219619P.

PR 03-NOV-2000; 2000US-0245157P.

PR 29-JAN-2001; 2001US-0264319P.

PR 21-MAR-2001; 2001US-0277270P.

XX (UTAH ) UNIV UTAH RES FOUND.

PA (COGN-) COGNETIX INC.

XX Olivera BM, McIntosh JM, Garrett JE, Watkins M, Cruz LJ, Shon K;

PI Jacobsen R, Jones RM, Cartier GS, Shen GS;

XX WPI; 2002-217020/27.

DR N-PSDB; ABL88542.

XX New mu-conopeptides useful for treating disorders associated with voltage

PT -gated sodium channels, e.g. stroke or pain, as neuromuscular blocking

PT agents, as local anesthetic agents, as analgesic agents and as

PT neuroprotective agents.

XX Claim 9; Page 52; 231pp; English.

PS The present invention relates to mu-conopeptides derived from snails,

CC which can be in the treatment of disorders associated with voltage-gated

CC ion channels. These may include neurodegenerative disorders such as

CC amyotrophic lateral sclerosis, neuromuscular disorders, post-operative or

CC severe chronic pain, stroke, trigeminal neuralgia, diabetic neuropathy,

CC post-herpetic neuralgia, neuronal pain and phantom limb, burn pain,

CC epilepsy, for reducing neurotoxic injury associated with hypoxia, anoxia

CC or ischaemia which typically follows stroke, cerebrovascular accident,

CC brain or spinal cord trauma, myocardial infarct, physical trauma,

CC drowning, suffocation, perinatal asphyxia, or hypoglycaemic events, for

CC providing muscle relaxation, treating essential blepharospasm and other

CC forms of focal dystonia, and for anti-wrinkle use. The present sequence

CC is a mu-conopeptide preprotein of the invention

XX Sequence 76 AA;

SQ Query Match 40.7%; Score 50; DB 5; Length 76;

Best Local Similarity 61.5%; Pred. No. 35;

Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 2 NWRCCILIPACRRN 14

Db 59 NLRCLCPVACRRN 71

RESULT 19

AAR75275

ID AAR75275 standard; peptide; 16 AA.

XX AAR75275;

XX 27-AUG-2003 (revised)

DT 21-DEC-1995 (first entry)

XX A-lineage conotoxin BN-2 peptide.

XX Conotoxin; neuromuscular; synapse; signal transmission; inhibitor.

XX Conus bandanus.

XX Key Location/Qualifiers

FT Misc-difference 6 /label= Pro or OTHER

FT /note= "Hydroxyproline"

FT Misc-difference 13 /label= Pro or OTHER

FT /note= "Hydroxyproline"

FT Modified-site 16 /note= "preferably amidated"

FT

WO9511256-A1.  
27-APR-1995.  
19-OCT-1994; 94WO-US011927.  
19-OCT-1993; 93US-00137800.  
(UTAH ) UNIV UTAH RES FOUND.  
Olivera BM, Cruz LJ, Hillyard DR, McIntosh JM, Santos AD;  
WPI; 1995-170189/22.  
New A-lineage conotoxin peptide(s) - which inhibit synaptic transmission at the neuromuscular junction or are active against potassium or sodium channels.  
Claim 1; Page 42; 66pp; English.  
The kappa-conotoxin, alpha conotoxin and alpha-like conotoxin peptides all belong to a group of peptides known as the A-lineage conotoxin peptides. The A-lineage conotoxin peptides have a wide variety of pharmacological uses. The A-lineage conotoxin peptides claimed (AAR75264-75293) are useful for the inhibition of synaptic transmission at neuromuscular junctions by blocking nicotinic acetyl choline receptors and they also have activity against voltage-gated Na and K channels.  
(Updated on 27-AUG-2003 to correct OS field.)  
Sequence 16 AA;  
Query Match 39.8%; Score 49; DB 2; Length 16;  
Best Local Similarity 46.7%; Pred. No. 13;  
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;  
5 CCLIPACRRNHKKFC 19  
||| : : :  
2 CCTHPACHVSHPELC 16  
SULT 20  
WZ4882  
AAW24882 standard; peptide; 16 AA.  
AAW24882;  
25-MAR-2003 (revised)  
15-OCT-1997 (first entry)  
Predatory cone snail venom alpha-conotoxin BN-2.  
Conotoxin; venom; predatory; cone snail; Conus; A-lineage; inhibitor;  
synaptic transmission; neuromuscular junction; block; alpha-conotoxin;  
nicotinic acetylcholine receptor; kappa-conotoxin;  
voltage-sensitive potassium CHANNEL; sodium channel.  
Conus bandanus.  
Key Location/Qualifiers  
Modified-site 6  
/note= "optionally may be 4Hyp"  
Modified-site 13  
/note= "optionally may be 4Hyp"  
Modified-site 16  
/note= "amidated C-terminus"  
US5633347-A.  
27-MAY-1997.  
07-JUN-1995; 95US-00480750.  
29-JUN-1993; 93US-00084848.  
19-OCT-1993; 93US-00137800.  
29-JUN-1993; 93US-00084848.  
19-OCT-1993; 93US-00137800.  
(UTAH ) UNIV UTAH RES FOUND.  
Hillyard DR, Cruz LJ, McIntosh JM, Santos AO, Olivera BM;  
WPI; 1997-309336/28.  
New kappa-conotoxin peptide(s) - present in venom of fish-hunting cone snail.  
Disclosure; Col 5; 37pp; English.  
The peptides AAW24878-W24900 represent novel toxin peptides isolated from the venom of various predatory cone snails of the genus Conus. The peptides are A-lineage conotoxin peptides which fall into 3 groups dependent on their amino acid sequences: (i) alpha-3/5 have a core sequence CXXXXXXXXC where X is any amino acid; (ii) alpha-4/7 have a core sequence CXXXXXXXCXCC; and (iii) kappa-7/21/3 have the core sequence CXXXXXXXCXCCXXC. The peptide presented here was isolated from Conus bandanus and falls into the alpha-4/7 category. Alpha-conotoxin peptides are potent inhibitors of synaptic transmission at the neuromuscular junction by blocking nicotinic acetylcholine receptors, whereas kappa-conotoxins have activities against voltage-sensitive potassium or sodium channels. (Updated on 25-MAR-2003 to correct PF field.)  
Sequence 16 AA;  
Query Match 39.8%; Score 49; DB 2; Length 16;  
Best Local Similarity 46.7%; Pred. No. 13;  
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;  
5 CCLIPACRRNHKKFC 19  
||| : : :  
2 CCTHPACHVSHPELC 16  
RESULT 21  
AAW12737  
ID AAW12737 standard; peptide; 16 AA.  
XX  
AC AAW12737;  
XX  
DT 25-MAR-2003 (revised)  
DT 16-APR-1997 (first entry)  
XX  
DE A-lineage conotoxin peptide BN-2.  
XX  
KW Polymerase chain reaction; PCR; primer; amplify; conotoxin; Conus;  
KW inhibitor; synaptic transmission; neuromuscular junction; sodium channel;  
KW nicotinic acetylcholine receptor; potassium channel; muscle relaxant;  
KW myasthenia gravis; small cell lung cancer; therapy.  
XX  
OS Conus bandanus.  
XX  
Key Location/Qualifiers  
Modified-site 6  
/note= "optionally hydroxylated"  
Modified-site 13  
/note= "optionally hydroxylated"  
Modified-site 15  
/note= "amidated"  
US5589340-A.  
31-DEC-1996.  
07-JUN-1995; 95US-00477383.  
29-JUN-1993; 93US-00084848.  
19-OCT-1993; 93US-00137800.

(UTAH ) UNIV UTAH RES FOUND.

Santos AD, Hillyard DR, McIntosh JM, Olivera BM, Cruz LJ;

WPI; 1997-076840/07.

Identifying nucleic acid encoding A-lineage conotoxin peptide(s) by amplification - uses primers corresponding to conserved regions in the signal sequence and 3'-untranslated regions, useful e.g. in treatment of small cell lung cancer.

Disclosure; Col 5; 36pp; English.

AAW12726-W12769 represent conotoxin peptides. This sequence represents the A-lineage conotoxin BN-2 peptide isolated from *Conus bandanus*. These sequences are identified using the method of the invention. The method of the invention is for identifying DNA encoding A-lineage conotoxin peptides by subjecting *Conus* nucleic acid to amplification with primer sequences (see AAT59714 and AAT59715). The primers are specific for the signal sequence and 3'-untranslated (3'UTR) regions of the conotoxin gene, which are highly homologous between conotoxins, and are therefore suitable sites for detection. A-lineage conotoxins include alpha-conotoxins, and kappa-conotoxins. Alpha-conotoxins are powerful inhibitors of synaptic transmission at the neuromuscular junction, and are usually nicotinic acetylcholine receptor blockers. Kappa-conotoxins act on the voltage sensitive sodium and potassium channels. The conotoxins identified can be used as muscle relaxants, in the diagnosis of myasthenia gravis, and for the treatment or diagnosis of small cell lung cancer. For the treatment of small cell lung cancer, the conotoxin peptides act by binding to the nicotinic receptors, and thereby blocking the nicotine/cytosine stimulated release of the mitogen 5-hydroxytryptamine. (Updated on 25-MAR-2003 to correct PF field.)

Sequence 16 AA;

Query Match 39.8%; Score 49; DB 2; Length 16;

Best Local Similarity 46.7%; Pred. No. 13;

Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

5 CCLIPACRRNHKKFC 19

2 CCTHFACHVSHPELC 16

ABP60018 standard; peptide; 16 AA.

ABP60018;

24-FEB-2003 (first entry)

Alpha-conotoxin peptide An1.1.

Alpha-conotoxin; cerebroprotective; analgesic; anticonvulsant; neuroleptic; antiparkinsonian; cytostatic; nontropic; neuroprotective; neuronal nicotinic acetylcholine receptor; NACHR; inhibitor; stroke; pain; cancer related pain; post-surgical pain; oral pain; referred trigeminal neuralgia; post-herpetic neuralgia; phantom limb pain; fibromyalgia; reflex sympathetic dystrophy; rheumatoid arthritis; inflammatory arthritis; neurogenic pain; neuropathic pain; epilepsy; nicotine addiction; schizophrenia; Parkinson's disease; small cell lung carcinoma; Alzheimer's disease; nerve injury.

Conus anemone.

Key Location/Qualifiers

Modified-site 16

/note= "C-terminal amide"

WO200279236-A1.

XX 10-OCT-2002.

XX 28-MAR-2002; 2002WO-AU000411.

XX 29-MAR-2001; 2001AU-00004094.

XX (LIVE/) LIVETT B.

XX (KHAL/) KHALIL Z.

XX (GAYL/) GAYLER K.

XX (DOWN/) DOWN J.

XX Livett B, Khalil Z, Gayler K, Down J;

XX WPI; 2003-103260/09.

New alpha- conotoxin-like peptides that inhibit the activity of neuronal nicotinic acetylcholine receptor, useful for treating stroke, pain, schizophrenia, Parkinson's disease, small cell lung carcinoma or Alzheimer's disease.

XX Claim 9; Page 57; 87pp; English.

The invention relates to an isolated alpha-conotoxin-like peptide sequence. The activity of peptides of the invention may be described as cerebroprotective, analgesic, anticonvulsant, neuroleptic, antiparkinsonian, cytostatic, nontropic and neuroprotective. Peptides of the invention are neuronal nicotinic acetylcholine receptor (NACHR) inhibitors. The alpha-conotoxin-like peptide is useful for treating a condition mediated by a neuronal nicotinic acetylcholine receptor, e.g. stroke, pain (e.g. cancer related pain, post-surgical pain, oral or dental pain, referred trigeminal neuralgia, post-herpetic neuralgia, phantom limb pain, fibromyalgia, reflex sympathetic dystrophy, pain associated with inflammatory conditions, rheumatoid arthritis or inflammatory arthritis, or pain resulting from conditions associated with neurogenic or neuropathic pain), epilepsy, nicotine addiction, schizophrenia, Parkinson's disease, small cell lung carcinoma, or Alzheimer's disease. The alpha-conotoxin-like peptide is also useful for accelerating recovery from nerve injury. The peptides are also useful as research reagents for investigating nicotinic acetylcholine receptor physiology and pharmacology. The current sequence represents an alpha-conotoxin peptide of the invention that has been designated An1.1

XX Sequence 16 AA;

SULT 22

P60018

Query Match 39.8%; Score 49; DB 6; Length 16;

Best Local Similarity 46.7%; Pred. No. 13;

Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 5 CCLIPACRRNHKKFC 19

Db 2 CSHFACVANNQDYC 16

RESULT 23

ABG99820  
ID ABG99820 standard; peptide; 17 AA.

XX AC ABG99820;

XX 17-JAN-2003 (first entry)

XX Conus sp conotoxin-associated peptide SEQ ID 605.

XX Conotoxin; cone snail; analgesic; voltage-gated ion channel modulator;  
KW ligand-gated ion channel modulator; pain-relief.

XX Conus bandanus.

XX WO200264740-A2.

XX 22-AUG-2002.

XX PD

11-FEB-2002; 2002WO-US003887.

09-FEB-2001; 2001US-0267408P.

(COGN-) COGNETIX INC.

(UTAH ) UNIV UTAH RES FOUND.

Olivera BM, McIntosh JM, Watkins M, Garrett JE, Cruz LJ;  
Grilley M, Walker CS, Shetty R, Jones RM, Schoenfeld RM;

WPI; 2002-706921/76.

New cone snail conotoxin peptides, useful as a pain reliever for alleviating pain in an individual suffering from pain or who is about to be subjected to a pain-causing event, or for treating voltage-gated ion channel disorders.

Claim 1; Page 298-299; 305pp; English.

This invention describes novel conotoxin peptides from the cone snail, genus *Conus* which have analgesic activity and can act as a voltage-gated ion channel modulator or a ligand-gated ion channel modulator. The conotoxin peptide is useful as a pain-relieving agent for alleviating pain in an individual who is either exhibiting pain or is about to be subjected to a pain-causing event. The conotoxin peptide is also useful for treating or preventing disorders associated with voltage-gated ion channel disorders, ligand-gated ion channel disorders or receptor disorders. The radio-labeled conotoxin peptide is also useful for characterizing a new site on these receptors or channels, and for screening and identifying novel small molecules that interact with the above-mentioned channels or receptors, which are monoamine transporters. ABG9360-ABG99853 represent the conotoxin protein and peptides described in the disclosure of the invention

Sequence 17 AA;

Query Match 39.8%; Score 49; DB 5; Length 17;

Best Local Similarity 46.7%; Pred. No. 14;

Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

5 CCLIPACRRNHKFC 19

3 CCTHPACHVSHPELC 17

SULT 24

B21436

AB21436 standard; peptide; 18 AA.

AB21436;

19-JAN-2001 (first entry)

Cone snail alpha-conotoxin SEQ ID NO: 79.

Cone snail; alpha-conotoxin; venom; disulphide bond; mood disorder; neuronal nicotinic acetylcholine receptor; cardiovascular disorder; gastric motility disorder; urinary incontinence; nicotine addiction; small cell lung carcinoma.

*Conus bandanus*.

WO200044776-A1.

03-AUG-2000.

28-JAN-2000; 2000WO-US001979.

29-JAN-1999; 99US-0118381P.

(UTAH ) UNIV UTAH RES FOUND.

(COGN-) COGNETIX INC.

Watkins M, Olivera BM, Hillyard DR, McIntosh JM, Jones RM;

WPI; 2000-505965/45.

N-PSDB; AAA89411.

alpha-conotoxin polypeptides derived from the venom of cone snails useful e.g. as neuromuscular blocking agents for use in surgery and for treating unipolar depression.

Claim 39; Page 34; 229pp; English.

The present invention relates to a number of alpha-conotoxin peptides and their coding sequences from a number of different species of cone snails. These peptides are found in minute quantities in the venom of the snails, and are targeted at the neuronal nicotinic acetylcholine receptors of the nervous system. They usually contain two disulphide bonds which give them defined conformations, a rarity in molecules this small. The alpha-conotoxins can be used as neuromuscular blocking agents in surgery, and for treating disorders regulated at the neuronal nicotinic acetylcholine receptors, including cardiovascular disorders, gastric motility disorders, urinary incontinence, nicotine addiction, mood disorders such as bipolar disorder, unipolar depression, dysthymia and seasonal affective disorder, and small cell lung carcinoma

Sequence 18 AA;

Query Match 39.8%; Score 49; DB 3; Length 18;

Best Local Similarity 46.7%; Pred. No. 14;

Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 5 CCLIPACRRNHKFC 19

3 CCTHPACHVSHPELC 17

Db

RESULT 25

AB21617

ID AAB21617 standard; peptide; 25 AA.

XX

AC AAB21617;

XX 19-JAN-2001 (first entry)

XX Cone snail alpha-conotoxin SEQ ID NO: 362.

XX Cone snail; alpha-conotoxin; venom; disulphide bond; mood disorder; neuronal nicotinic acetylcholine receptor; cardiovascular disorder; gastric motility disorder; urinary incontinence; nicotine addiction; small cell lung carcinoma.

XX *Conus omaria*.

XX WO200044776-A1.

XX 03-AUG-2000.

XX 28-JAN-2000; 2000WO-US001979.

XX 29-JAN-1999; 99US-0118381P.

XX (UTAH ) UNIV UTAH RES FOUND.

XX (COGN-) COGNETIX INC.

XX Watkins M, Olivera BM, Hillyard DR, McIntosh JM, Jones RM;

XX WPI; 2000-505965/45.

XX N-PSDB; AAA89513.

XX alpha-conotoxin polypeptides derived from the venom of cone snails useful e.g. as neuromuscular blocking agents for use in surgery and for treating unipolar depression.

XX Claim 39; Page 61; 229pp; English.

The present invention relates to a number of alpha-conotoxin peptides and their coding sequences from a number of different species of cone snail. These peptides are found in minute quantities in the venom of the snails, and are targeted at the neuronal nicotinic acetylcholine receptors of the nervous system. They usually contain two disulphide bonds, which give them defined conformations, a rarity in molecules this small. The alpha-conotoxins can be used as neuromuscular blocking agents in surgery, and for treating disorders regulated at the neuronal nicotinic acetylcholine receptors, including cardiovascular disorders, gastric motility disorders, urinary incontinence, nicotine addiction, mood disorders such as bipolar disorder, unipolar depression, dysthymia and seasonal affective disorder, and small cell lung carcinoma

Sequence 25 AA;

Query Match 39.8%; Score 49; DB 3; Length 25;  
Best Local Similarity 46.7%; Pred. No. 19;  
Matches 7; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

5 CCLIPACRRNHKKFC 19  
||| ||| : : :  
7 CCSYPDCGANHPEIC 21

HULT 26

399639  
ABG99639 standard; protein; 60 AA.

ABG99639;

17-JAN-2003 (first entry)

Conus sp conotoxin-associated protein SEQ ID 409.

Conotoxin; cone snail; analgesic; voltage-gated ion channel modulator;  
ligand-gated ion channel modulator; pain-relief.

Conus bandanus.

WO200264740-A2.

22-AUG-2002.

11-FEB-2002; 2002WO-US003887.

09-FEB-2001; 2001US-0267408P.

(COGN-) COGNETIX INC.

(UTAH) UNIV UTAH RES FOUND.

Olivera BM, McIntosh JM, Watkins M, Garrett JE, Cruz LJ;  
Grille M, Walker CS, Shetty R, Jones RM, Schoenfeld RM;

WPI; 2002-706921/76.

N-PSDB; ABX04955.

New cone snail conotoxin peptides, useful as a pain reliever for  
alleviating pain in an individual suffering from pain or who is about to  
be subjected to a pain-causing event, or for treating voltage-gated ion  
channel disorders.

Claim 1; Page 257; 305pp; English.

This invention describes novel conotoxin peptides from the cone snail,  
genus Conus which have analgesic activity and can act as a voltage-gated  
ion channel modulator or a ligand-gated ion channel modulator. The  
conotoxin peptide is useful as a pain-relieving agent for alleviating  
pain in an individual who is either exhibiting pain or is about to be  
subjected to a pain-causing event. The conotoxin peptide is also useful  
for treating or preventing disorders associated with voltage-gated ion  
channel disorders, ligand-gated ion channel disorders or receptor  
disorders. The radiolabeled conotoxin peptide is also useful for

CC characterising a new site on these receptors or channels, and for  
CC screening and identifying novel small molecules that interact with the  
CC above-mentioned channels or receptors, which are monoamine transporters.  
CC ABG99639-ABG99853 represent the conotoxin protein and peptides described  
CC in the disclosure of the invention

XX Sequence 60 AA;

Query Match 39.8%; Score 49; DB 5; Length 60;

Best Local Similarity 46.7%; Pred. No. 39;

Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 5 CCLIPACRRNHKKFC 19

||| ||| : : :  
Db 45 CCHPACHVSHPELC 59

RESULT 27

AA21431  
ID AA21431 standard; protein; 61 AA.

XX AC AA21431;

XX DT 19-JAN-2001 (first entry)

XX DE Cone snail alpha-conotoxin SEQ ID NO: 69.

XX KW Cone snail; alpha-conotoxin; venom; disulphide bond; mood disorder;  
KW neuronal nicotinic acetylcholine receptor; cardiovascular disorder;  
KW gastric motility disorder; urinary incontinence; nicotine addiction;  
KW small cell lung carcinoma.

XX OS Conus textile.

XX PN WO200044776-A1.

XX PD 03-AUG-2000.

XX PF 28-JAN-2000; 2000WO-US001979.

XX PR 29-JAN-1999; 99US-0118381P.

XX PA (UTAH) UNIV UTAH RES FOUND.

XX PA (COGN-) COGNETIX INC.

XX PI Watkins M, Olivera BM, Hillyard DR, McIntosh JM, Jones RM;

XX DR WPI; 2000-505965/45.

XX DR N-PSDB; AAA89406.

PT alpha-conotoxin polypeptides derived from the venom of cone snails useful  
e.g. as neuromuscular blocking agents for use in surgery and for treating  
unipolar depression.

XX Claim 39; Page 33; 229pp; English.

XX The present invention relates to a number of alpha-conotoxin peptides and  
their coding sequences from a number of different species of cone snail.  
These peptides are found in minute quantities in the venom of the snails,  
and are targeted at the neuronal nicotinic acetylcholine receptors of the  
nervous system. They usually contain two disulphide bonds, which give  
them defined conformations, a rarity in molecules this small. The alpha-  
conotoxins can be used as neuromuscular blocking agents in surgery, and  
for treating disorders regulated at the neuronal nicotinic acetylcholine  
receptors, including cardiovascular disorders, gastric motility  
disorders, urinary incontinence, nicotine addiction, mood disorders such  
as bipolar disorder, unipolar depression, dysthymia and seasonal  
affective disorder, and small cell lung carcinoma

XX Sequence 61 AA;

Query Match 39.8%; Score 49; DB 3; Length 61;

Best Local Similarity 43.8%; Pred. No. 40;

Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

4 RCCLIPACRHHKFC 19  
:|||||:|:  
45 QCCSHPCNVDPHPEIC 60

SULT 28  
B21433  
AAB21433 standard; protein; 61 AA.  
AAB21433;  
19-JAN-2001 (first entry)  
Cone snail alpha-conotoxin SEQ ID NO: 73.  
Cone snail; alpha-conotoxin; venom; disulphide bond; mood disorder;  
neuronal nicotinic acetylcholine receptor; cardiovascular disorder;  
gastric motility disorder; urinary incontinence; nicotine addiction;  
small cell lung carcinoma.  
Conus radiatus.  
WO200044776-A1.  
03-AUG-2000.  
28-JAN-2000; 2000WO-US001979.  
29-JAN-1999; 99US-0118381P.  
(UTAH ) UNIV UTAH RES FOUND.  
(COGN-) COGNETIX INC.  
Watkins M, Olivera BW, Hillyard DR, McIntosh JM, Jones RM;  
WPI; 2000-505965/45.  
N-PSDB; AAB89408.  
alpha-conotoxin polypeptides derived from the venom of cone snails useful  
e.g. as neuromuscular blocking agents for use in surgery and for treating  
unipolar depression.  
Claim 39; Page 33-34; 229pp; English.  
The present invention relates to a number of alpha-conotoxin peptides and  
their coding sequences from a number of different species of cone snail.  
These peptides are found in minute quantities in the venom of the snails,  
and are targeted at the neuronal nicotinic acetylcholine receptors of the  
nervous system. They usually contain two disulphide bonds, which give  
them defined conformations, a rarity in molecules this small. The alpha-  
conotoxins can be used as neuromuscular blocking agents in surgery, and  
for treating disorders regulated at the neuronal nicotinic acetylcholine  
receptors, including cardiovascular disorders, gastric motility  
disorders, urinary incontinence, nicotine addiction, mood disorders such  
as bipolar disorder, unipolar depression, dysthymia and seasonal  
affective disorder, and small cell lung carcinoma

Sequence 61 AA;  
Query Match 39.8%; Score 49; DB 3; Length 61;  
Best Local Similarity 43.8%; Pred. No. 40;  
Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

4 RCCLIPACRHHKFC 19  
:|||||:|:  
45 QCCSHPCNVDPHPEIC 60

SULT 29  
G11969  
ABG11969 standard; protein; 747 AA.

XX ABG11969;  
XX 18-FEB-2002 (first entry)  
XX Novel human diagnostic protein #11960.  
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;  
KW food supplement; medical imaging; diagnostic; genetic disorder.  
XX Homo sapiens.  
XX WO200175067-A2.  
XX 11-OCT-2001.  
XX 30-MAR-2001; 2001WO-US008631.  
XX 31-MAR-2000; 2000US-00540217.  
PR 23-AUG-2000; 2000US-00849167.  
XX (HYSE-) HYSEQ INC.  
XX Drmanac RT, Liu C, Tang YT;  
XX WPI; 2001-639362/73.  
XX N-PSDB; AAS76156.  
XX New isolated polynucleotide and encoded polypeptides, useful in  
PT diagnostics, forensics, gene mapping, identification of mutations  
PT responsible for genetic disorders or other traits and to assess  
PT biodiversity.  
XX Claim 20; SEQ ID NO 42328; 103pp; English.  
XX The invention relates to isolated polynucleotide (I) and polypeptide (II)  
CC sequences. (I) is useful as hybridisation probes, polymerase chain  
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,  
CC and in recombinant production of (II). The polynucleotides are also used  
CC in diagnostics as expressed sequence tags for identifying expressed  
CC genes. (II) is useful in gene therapy techniques to restore normal  
CC activity of (II) or to treat disease states involving (II). (II) is  
CC useful for generating antibodies against it, detecting or quantitating a  
CC polypeptide in tissue, as molecular weight markers and as a food  
CC supplement. (II) and its binding partners are useful in medical imaging  
CC of sites expressing (II). (I) and (II) are useful for treating disorders  
CC involving aberrant protein expression or biological activity. The  
CC polypeptide and polynucleotide sequences have applications in  
CC diagnostics, forensics, gene mapping, identification of mutations  
CC responsible for genetic disorders or other traits to assess biodiversity  
CC and to produce other types of data and products dependent on DNA and  
CC amino acid sequences. ABG0010-ABG30377 represent novel human diagnostic  
CC amino acid sequences of the invention. Note: The sequence data for this  
CC patent did not appear in the printed specification, but was obtained in  
CC electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pat\_sequences  
XX Sequence 747 AA;  
SQ

Query Match 39.8%; Score 49; DB 4; Length 747;  
Best Local Similarity 66.7%; Pred. No. 3.2e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FNRCCCLIP 9  
:|||||:  
Db 161 YNNCCCFIP 169

RESULT 30  
AAY24163  
ID AAY24163 standard; peptide; 16 AA.  
XX  
AC AAY24163;

10-SEP-1999 (first entry)

Alpha-conotoxin peptide SEQ ID NO:9.

Alpha-conotoxin; neuronal nicotinic acetylcholine receptor; nAChR; small cell lung carcinoma; cardiovascular disorder; nicotine addiction; gastric motility disorder; urinary incontinence; mood disorder; bipolar disorder; unipolar depression; dysthymia; seasonal affective disorder.

Conus purpurascens.

WO9933482-A1.

08-JUL-1999.

23-DEC-1998; 98WO-US027367.

31-DEC-1997; 97US-0070153P.

03-APR-1998; 98US-0060588P.

(UTAH ) UNIV UTAH RES FOUND.

Olivera BM, McIntosh JM, Yoshikami D, Cartier GE, Luo S;

WPI; 1999-405367/34.

Alpha-conotoxin peptides that are used to treat disorders regulated at neuronal nicotinic acetylcholine receptors.

Claim 28; Page 6; 40pp; English.

The present sequence represents a specifically claimed example of an alpha-conotoxin, which can be used to treat disorders regulated at neuronal nicotinic acetylcholine receptors (nAChR). The alpha-conotoxins are useful for preparing a pharmaceutical composition for treating disorders regulated at neuronal nAChR, especially alpha 3 beta 2, alpha 3 beta 4 or alpha 7-containing nAChR. Disorders that can be treated include cardiovascular disorders, a gastric motility disorder, urinary incontinence, nicotine addiction, a mood disorder or small cell lung carcinoma. Mood disorders include bipolar disorder, unipolar depression, dysthymia and seasonal affective disorder. The alpha- conotoxins can also be used for diagnosis of small cell lung carcinoma. The alpha-conotoxin antagonists are able to discriminate between non- symmetrical ligand binding interfaces present on the nAChR. The alpha- conotoxin has the ability to potentially block any receptor containing a alpha beta subunit interface, regardless of what other subunits may be present in the receptor complex

Sequence 16 AA;

Query Match 39.0%; Score 48; DB 2; Length 16;  
Best Local Similarity 40.0%; Pred. No. 17;  
Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

5 CCLIPACRRNHKKFC 19.

2 CCSLPFCAANNPDYC 16

ULT 31  
24887

AAW24887 standard; peptide; 18 AA.

AAW24887;

25-MAR-2003 (revised)

15-OCT-1997 (first entry)

Predatory cone snail venom alpha-conotoxin SL-1.

Conotoxin; venom; predatory; cone snail; Conus; A-lineage; inhibitor;

KW synaptic transmission; neuromuscular junction; block; alpha-conotoxin;  
KW nicotinic acetylcholine receptor; kappa-conotoxin;  
KW voltage-sensitive potassium CHANNEL; sodium channel.

OS Conus sulcatus.

XX Key Location/Qualifiers

XX Modified-site 7

FT /note= "optionally 4Hyp"

FT Modified-site 14

FT /note= "optionally 4Hyp"

FT Misc-difference 15

FT /label= Glu, OTHER

FT /note= "OTHER = gamma-carboxyglutamate (Glu)"

FT Modified-site 18

FT /note= "amidated C-terminus"

XX US5633347-A.

XX 27-MAY-1997.

XX 07-JUN-1995; 95US-00480750.

XX 29-JUN-1993; 93US-00084848.

PR 19-OCT-1993; 93US-00137800.

XX (UTAH ) UNIV UTAH RES FOUND.

XX Hillyard DR, Cruz LJ, McIntosh JM, Santos AO, Olivera BM;

XX WPI; 1997-309336/28.

XX New kappa-conotoxin peptide(s) - present in venom of fish-hunting cone snail.

XX Disclosure; Col 5; 37pp; English.

XX The peptides AAW24878-W24900 represent novel toxin peptides isolated from the venom of various predatory cone snails of the genus Conus. The peptides are A-lineage conotoxin peptides which fall into 3 groups dependent on their amino acid sequences: (i) alpha-3/5 have a core sequence CCXXXCXXXXC where X is any amino acid; (ii) alpha-4/7 have a core sequence CCXXXCXXXXC; and (iii) kappa-7/2/1/3 have the core sequence CCXXXXXXCXCCXXXC. The peptide presented here was isolated from Conus sulcatus and falls into the alpha-4/7 category. Alpha-conotoxin peptides are potent inhibitors of synaptic transmission at the neuromuscular junction by blocking nicotinic acetylcholine receptors, whereas kappa-conotoxins have activities against voltage-sensitive potassium or sodium channels. (Updated on 25-MAR-2003 to correct PF field.)

XX Sequence 18 AA;

Query Match 39.0%; Score 48; DB 2; Length 18;  
Best Local Similarity 46.7%; Pred. No. 19;  
Matches 7; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Qy 5 CCLIPACRRNHKKFC 19

Db 3 CCSFPACRRKYPXMC 17

RESULT 32

AAW24887

ID AAW24887 standard; peptide; 18 AA.

XX AAW24887;

XX 18-JUL-2000 (first entry)

XX Mature conotoxin peptide #2.

XX Mature conotoxin; brocade cone shell; line cone shell; drug screening;

neuronal inhibitor; muscle inhibitor.

Conus sp.

CN1237584-A.

08-DEC-1999.

30-APR-1999; 99CN-00106070.

30-APR-1999; 99CN-00106070.

(BIOL-) BIOLOGICAL ENG INST ACAD MILITARY MEDICI.

Lu B, Huang P;

WPI; 2000-351193/31.

Conotoxin peptide from brocade, cone shells useful as analgesic.

Claim 1A; Page 2; 20pp; Chinese.

The invention relates to 14 novel mature conotoxin peptides from marine snails (Conus species); conotoxin precursor proteins; and cDNAs encoding the conotoxin precursors. The mature peptide sequences were discovered by obtaining conotoxin cDNA sequences from mRNA from the brocade cone shell (Conus textile) or the line cone shell (Conus striatus). The cDNA sequences were used to determine the conotoxin precursor protein sequences, and the sequences of the mature conotoxin peptides were inferred from the precursor sequences. The mature conotoxin peptides can be obtained via chemical synthesis or by in vitro gene expression. Conotoxins inhibit the function of neurons and muscle cells. Certain conotoxins interfere with synaptic transmission, while others act on muscle or at the neuromuscular junction. The 14 novel conotoxins have unique receptor specificity and affinity, so can be used as screening tools to identify new drugs. Conotoxin #11 (AAV87524) may be used for pain relief. Sequences AAV87420, AAV87524, AAV87526, AAV87528, AAV87530, AAV87532, AAV87534, AAV87536, AAV87538, AAV87540, AAV87542, AAV87544 and AAV87546 represent mature conotoxins #1-#14, respectively

Sequence 18 AA;

Query Match 39.0%; Score 48; DB 3; Length 18;  
Best Local Similarity 46.7%; Pred. No. 19;  
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

5 CCLIPACRRNHKKFC 19  
||| ||| : : :  
3 CCHPACNVDPHEIC 17

MULT 33

321523

AAB21523 standard; peptide; 18 AA.

AAB21523;

22-JAN-2001 (first entry)

Cone snail alpha-conotoxin SEQ ID NO: 203.

Cone snail; alpha-conotoxin; venom; disulphide bond; mood disorder;  
neuronal nicotinic acetylcholine receptor; cardiovascular disorder;  
gastric motility disorder; urinary incontinence; nicotine addiction;  
small cell lung carcinoma.

Conus musicus.

Key Location/Qualifiers

Misc-difference 2

/label= Lys, OTHER  
/note= "N-methyl-Lys, N,N-dimethyl-Lys or N,N,N-trimethyl-Lys"

Misc-difference 12  
/label= Lys, OTHER  
/note= "N-methyl-Lys, N,N-dimethyl-Lys or N,N,N-trimethyl-Lys"

Misc-difference 14  
/label= Pro, OTHER  
/note= "hydroxy-Pro"

Misc-difference 16  
/label= Tyr, OTHER  
/note= "mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr or nitro-Tyr"

WC200044776-A1.

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WO200044776-A1.

03-AUG-2000.

28-JAN-2000; 2000WO-US001979.

29-JAN-1999; 99US-0118381P.

(UTAH ) UNIV UTAH RES FOUND.  
(COGN-) COGNETIX INC.

Watkins M, Olivera BM, Hillyard DR, McIntosh JM, Jones RM;

WPI; 2000-505965/45.  
N-PSDB; AAA89530.

alpha-conotoxin polypeptides derived from the venom of cone snails useful e.g. as neuromuscular blocking agents for use in surgery and for treating unipolar depression.

Claim 39; Page 65; 229pp; English.

The present invention relates to a number of alpha-conotoxin peptides and their coding sequences from a number of different species of cone snail. These peptides are found in minute quantities in the venom of the snails, and are targeted at the neuronal nicotinic acetylcholine receptors of the nervous system. They usually contain two disulphide bonds, which give them defined conformations, a rarity in molecules this small. The alpha-conotoxins can be used as neuromuscular blocking agents in surgery, and for treating disorders regulated at the neuronal nicotinic acetylcholine receptors, including cardiovascular disorders, gastric motility disorders, urinary incontinence, nicotine addiction, mood disorders such as bipolar disorder, unipolar depression, dysthymia and seasonal affective disorder, and small cell lung carcinoma

Sequence 38 AA;

Query Match 39.0%; Score 48; DB 3; Length 38;  
est Local Similarity 46.7%; Pred. No. 36;  
atches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

5 CCLIPACRRNHKKFC 19  
||| : : :  
23 CCSHPACNVDPHPC 37

ULT 35  
21586

AA821586 standard; peptide; 39 AA.

AA821586;

19-JAN-2001 (first entry)

Cone snail alpha-conotoxin SEQ ID NO: 300.

Cone snail; alpha-conotoxin; venom; disulphide bond; mood disorder; neuronal nicotinic acetylcholine receptor; cardiovascular disorder; gastric motility disorder; urinary incontinence; nicotine addiction; small cell lung carcinoma.

Conus arenatus.

WO200044776-A1.

03-AUG-2000.

28-JAN-2000; 2000WO-US001979.

29-JAN-1999; 99US-0118381P.

(UTAH ) UNIV UTAH RES FOUND.

PA (COGN-) COGNETIX INC.

XX Watkins M, Olivera BM, Hillyard DR, McIntosh JM, Jones RM;

PI WPI; 2000-505965/45.

XX N-PSDB; AAA89482.

PT alpha-conotoxin polypeptides derived from the venom of cone snails useful e.g. as neuromuscular blocking agents for use in surgery and for treating unipolar depression.

XX Claim 39; Page 54; 229pp; English.

XX The present invention relates to a number of alpha-conotoxin peptides and their coding sequences from a number of different species of cone snail. These peptides are found in minute quantities in the venom of the snails, and are targeted at the neuronal nicotinic acetylcholine receptors of the nervous system. They usually contain two disulphide bonds, which give them defined conformations, a rarity in molecules this small. The alpha-conotoxins can be used as neuromuscular blocking agents in surgery, and for treating disorders regulated at the neuronal nicotinic acetylcholine receptors, including cardiovascular disorders, gastric motility disorders, urinary incontinence, nicotine addiction, mood disorders such as bipolar disorder, unipolar depression, dysthymia and seasonal affective disorder, and small cell lung carcinoma

SQ Sequence 39 AA;

Query Match 39.0%; Score 48; DB 3; Length 39;  
Best Local Similarity 53.3%; Pred. No. 37;  
Matches 8; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 5 CCLIPACRRNHKKFC 19

Db 22 CCSNPACRVNPHVC 36

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Job time : 97 secs

GenCore version 5.1.6  
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protein - protein search, using sw model

on: February 18, 2004, 06:07:14 ; Search time 608 Seconds

(without alignments)  
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Maximum Match 100%

Listing first 50 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

ult No.	Score	Match	Length	DB	ID	Description
1	50	40.7	76	10	US-09-910-009A-189	Sequence 189, App
2	49.5	40.2	25	15	US-10-430-545-2	Sequence 2, Appli
3	49	39.8	17	14	US-10-072-602B-605	Sequence 605, App
4	49	39.8	60	14	US-10-072-602B-409	Sequence 409, App
5	48	39.0	16	9	US-09-897-465-9	Sequence 9, Appli
6	48	39.0	64	14	US-10-050-704-154	Sequence 154, App
7	48	39.0	76	9	US-09-764-847-511	Sequence 511, App
8	48	39.0	76	14	US-10-092-154-511	Sequence 511, App
9	48	39.0	150	9	US-09-915-582-63	Sequence 63, Appl
10	48	39.0	150	9	US-09-915-582-83	Sequence 83, Appl
11	48	39.0	150	10	US-09-832-129-49	Sequence 49, Appl
12	48	39.0	150	11	US-09-833-245-1472	Sequence 1472, Ap
13	48	39.0	150	11	US-09-833-245-1473	Sequence 1473, Ap
14	48	39.0	150	11	US-09-833-245-2227	Sequence 2227, Ap
15	48	39.0	150	14	US-10-050-704-182	Sequence 182, App

Sequence 63, Appl  
Sequence 89, Appl  
Sequence 61, Appl  
Sequence 158, App  
Sequence 601, App  
Sequence 774, App  
Sequence 1202, Ap  
Sequence 981, App  
Sequence 10, Appl  
Sequence 598, App  
Sequence 599, App  
Sequence 392, App  
Sequence 395, App  
Sequence 111, App  
Sequence 2498, Ap  
Sequence 153, App  
Sequence 152, App  
Sequence 428, App  
Sequence 89, Appl  
Sequence 349, App  
Sequence 568, App  
Sequence 608, App  
Sequence 220, App  
Sequence 278, App  
Sequence 17, Appl  
Sequence 17, Appl  
Sequence 17, Appl  
Sequence 17, Appl  
Sequence 6, Appli  
Sequence 17, Appl  
Sequence 1416, Ap  
Sequence 39, Appl  
Sequence 2, Appli  
Sequence 61-2, App

#### ALIGNMENTS

#### RESULT 1

US-09-910-009A-189  
Sequence 189, Application US/09910009A  
Publication No. US20030050234A1  
GENERAL INFORMATION:  
APPLICANT: University of Utah Research Foundation  
APPLICANT: Cognetix, Inc.  
APPLICANT: Oliveira, Baldomero M.  
APPLICANT: McIntosh, J. Michael  
APPLICANT: Garrett, James E.  
APPLICANT: Watkins, Maren  
APPLICANT: Cruz, Lourdes J.  
APPLICANT: Shon, Ki-Joon  
APPLICANT: Jacobsen, Richard  
APPLICANT: Jones, Robert M.  
APPLICANT: Cartier, G. Edward  
APPLICANT: Shen, Greg S.  
APPLICANT: Westaff, John D.  
TITLE OF INVENTION: Mu-Conopeptides  
FILE REFERENCE: 2314-242  
CURRENT APPLICATION NUMBER: US/09/910,009A  
CURRENT FILING DATE: 2001-07-23  
PRIOR APPLICATION NUMBER: US 60/219,619  
PRIOR FILING DATE: 2000-07-21  
PRIOR APPLICATION NUMBER: US 60/245,157  
PRIOR FILING DATE: 2000-11-03  
PRIOR APPLICATION NUMBER: US 60/264,319  
PRIOR FILING DATE: 2001-01-29  
PRIOR APPLICATION NUMBER: US 60/277,270  
PRIOR FILING DATE: 2001-03-21  
NUMBER OF SEQ ID NOS: 520  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 189

LENGTH: 76  
 TYPE: PRT  
 ORGANISM: Conus radiatus  
 09-910-009A-189  
 Query Match 40.7%; Score 50; DB 10; Length 76;  
 Best Local Similarity 61.5%; Pred. No. 14;  
 Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
 2 NRCLIPACRN 14  
 59 NRCLIPACRN 71  
 ULT 2  
 10-430-545-2  
 Sequence 2, Application US/10430545  
 Publication No. US20040014660A1  
 GENERAL INFORMATION:  
 APPLICANT: Daring, Matthew  
 APPLICANT: Collin, Haile  
 TITLE OF INVENTION: Insulin-Associated Peptides With Effects On Cerebral Health  
 FILE REFERENCE: 102182-34  
 CURRENT APPLICATION NUMBER: US/10/430,545  
 PRIOR FILING DATE: 2003-05-06  
 PRIOR APPLICATION NUMBER: 60/378,318  
 PRIOR FILING DATE: 2002-05-06  
 NUMBER OF SEQ ID NOS: 3  
 SOFTWARE: PatentIn version 3.0  
 SEQ ID NO 2  
 LENGTH: 25  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 10-430-545-2  
 Query Match 40.2%; Score 49.5; DB 15; Length 25;  
 Best Local Similarity 52.9%; Pred. No. 6.5;  
 Matches 9; Conservative 4; Mismatches 3; Indels 1; Gaps 1;  
 4 RCCLIPAC-RRNHKFC 19  
 9 KCCLIGACTKRSKLYC 25  
 SULT 3  
 10-072-602B-605  
 Sequence 605, Application US/10072602B  
 Publication No. US20030109670A1  
 GENERAL INFORMATION:  
 APPLICANT: University of Utah Research Foundation  
 APPLICANT: Cognetix, Inc.  
 APPLICANT: Olivera, Baldomero M.  
 APPLICANT: McIntosh, J. Michael  
 APPLICANT: Watkins, Maren  
 APPLICANT: Garrett, James E.  
 APPLICANT: Cruz, Lourdes J.  
 APPLICANT: Grilley, Michelle  
 APPLICANT: Schoenfeld, Robert M.  
 APPLICANT: Walker, Craig  
 APPLICANT: Shetty, Reshma  
 APPLICANT: Jones, Robert M.  
 TITLE OF INVENTION: Cone Snail Peptides  
 FILE REFERENCE: 2314-249  
 CURRENT APPLICATION NUMBER: US/10/072,602B  
 PRIOR FILING DATE: 2002-02-11  
 PRIOR APPLICATION NUMBER: US 60/267,408  
 NUMBER OF SEQ ID NOS: 638  
 SOFTWARE: PatentIn version 3.0  
 SEQ ID NO 605  
 LENGTH: 17  
 TYPE: PRT  
 ORGANISM: Conus bandanus

US-10-072-602B-605  
 Query Match 39.8%; Score 49; DB 14; Length 17;  
 Best Local Similarity 46.7%; Pred. No. 5.5;  
 Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;  
 QY 5 CCLIPACRRNHKFC 19  
 DB 3 CCTHPACHVSHPELC 17  
 RESULT 4  
 US-10-072-602B-409  
 Sequence 409, Application US/10072602B  
 Publication No. US20030109670A1  
 GENERAL INFORMATION:  
 APPLICANT: University of Utah Research Foundation  
 APPLICANT: Cognetix, Inc.  
 APPLICANT: Olivera, Baldomero M.  
 APPLICANT: McIntosh, J. Michael  
 APPLICANT: Watkins, Maren  
 APPLICANT: Garrett, James E.  
 APPLICANT: Cruz, Lourdes J.  
 APPLICANT: Grilley, Michelle  
 APPLICANT: Schoenfeld, Robert M.  
 APPLICANT: Walker, Craig  
 APPLICANT: Shetty, Reshma  
 APPLICANT: Jones, Robert M.  
 TITLE OF INVENTION: Cone Snail Peptides  
 FILE REFERENCE: 2314-249  
 CURRENT APPLICATION NUMBER: US/10/072,602B  
 PRIOR FILING DATE: 2002-02-11  
 PRIOR APPLICATION NUMBER: US 60/267,408  
 NUMBER OF SEQ ID NOS: 638  
 SOFTWARE: PatentIn version 3.0  
 SEQ ID NO 409  
 LENGTH: 60  
 TYPE: PRT  
 ORGANISM: Conus bandanus  
 US-10-072-602B-409  
 Query Match 39.8%; Score 49; DB 14; Length 60;  
 Best Local Similarity 46.7%; Pred. No. 16;  
 Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;  
 QY 5 CCLIPACRRNHKFC 19  
 DB 45 CCTHPACHVSHPELC 59  
 RESULT 5  
 US-09-897-465-9  
 Sequence 9, Application US/09897465  
 Patent No. US2002022715A1  
 GENERAL INFORMATION:  
 APPLICANT: Olivera, Baldomero M.  
 APPLICANT: McIntosh, J. Michael  
 APPLICANT: Yoshikami, Doju  
 APPLICANT: Cartier, G. Edward  
 APPLICANT: Luo, Siglin  
 APPLICANT: University of Utah Research Foundation  
 TITLE OF INVENTION: Uses of Alpha-Conotoxin Peptides  
 FILE REFERENCE: Uses of Alpha-Conotoxins  
 CURRENT APPLICATION NUMBER: US/09/897,465  
 CURRENT FILING DATE: 2001-07-03  
 PRIOR APPLICATION NUMBER: US 60/080,588  
 PRIOR FILING DATE: 1998-04-03  
 PRIOR APPLICATION NUMBER: US 60/070,153  
 PRIOR FILING DATE: 1997-12-31  
 NUMBER OF SEQ ID NOS: 13  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 9

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LENGTH: 16
TYPE: PRT
ORGANISM: Conus purpurascens
9-897-455-9

ery Match          39.0%; Score 48; DB 9; Length 16;
st Local Similarity 40.0%; Pred. No. 7.1;
tches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

5 CCLIPACRRNHKFC 19
||:|||||:|
2 CCSLPPCAANPDYC 16

LT 6
0-050-704-154
quence 154, Application US/10050704
blication No. US2003005042A1
NERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: 62 Human Secreted Proteins
FILE REFERENCE: P2039P1
CURRENT APPLICATION NUMBER: US/10/050,704
CURRENT FILING DATE: 2002-01-18
RIOR APPLICATION NUMBER: 09/684,524
RIOR FILING DATE: 2000-10-10
RIOR APPLICATION NUMBER: PCT/US00/08979
RIOR FILING DATE: 2000-04-06
RIOR APPLICATION NUMBER: 60/128,693
RIOR FILING DATE: 1999-04-09
RIOR APPLICATION NUMBER: 60/130,991
RIOR FILING DATE: 1999-04-26
NUMBER OF SEQ.ID NOS: 344
SOFTWARE: PatentIn Ver. 2.0
Q ID NO 154
LENGTH: 64
TYPE: PRT
ORGANISM: Homo sapiens
0-050-704-154

ery Match          39.0%; Score 48; DB 14; Length 64;
st Local Similarity 75.0%; Pred. No. 23;
tches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

2 NWRCCLP 9
||:|||||
39 NWKCCFP 46

LT 7
9-764-847-511
quence 511, Application US/09764847
tention No. US20020132767A1
NERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC009
CURRENT APPLICATION NUMBER: US/09/764,847
CURRENT FILING DATE: 2001-01-17
rior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 2003
SOFTWARE: PatentIn Ver. 2.0
Q ID NO 511
LENGTH: 76
TYPE: PRT
ORGANISM: Homo sapiens
9-764-847-511

ery Match          39.0%; Score 48; DB 9; Length 76;
st Local Similarity 53.8%; Pred. No. 26;
tches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

7 LIPACRRNHKFC 19

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Db          60 IVPKCRPHKEG 72      ::|||::|
RESULT 8
US-10-092-154-511
; Sequence 511, Application US/10092154
; Publication No. US20030054375A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC009C1
; CURRENT APPLICATION NUMBER: US/10/092,154
; CURRENT FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 2003
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 511
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-092-154-511
Query Match          39.0%; Score 48; DB 14; Length 76;
Best Local Similarity 53.8%; Pred. No. 26;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY          7 LIPACRNHKKFC 19      ::|||::|
Db          60 IVPKCRPHKEG 72      ::|||::|
RESULT 9
US-09-915-582-63
; Sequence 63, Application US/09915582
; Patent No. US20020120103A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 17 Human Secreted Proteins
; FILE REFERENCE: PS723P1
; CURRENT APPLICATION NUMBER: US/09/915,582
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: PCT/US01/01431
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/231,968
; PRIOR FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 63
; LENGTH: 150
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-915-582-63
Query Match          39.0%; Score 48; DB 9; Length 150;
Best Local Similarity 75.0%; Pred. No. 46;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY          2 NWRCCCLIP 9         ::|||
Db          125 NWKCCFIP 132      ::|||
RESULT 10
US-09-915-582-83
; Sequence 83, Application US/09915582
; Patent No. US20020120103A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.

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TITLE OF INVENTION: 17 Human Secreted Proteins  
FILE REFERENCE: PS723PI  
CURRENT APPLICATION NUMBER: US/09/915,582  
CURRENT FILING DATE: 2001-07-27  
PRIOR APPLICATION NUMBER: PCT/US01/01431  
PRIOR FILING DATE: 2001-01-17  
PRIOR APPLICATION NUMBER: 60/179,065  
PRIOR FILING DATE: 2000-01-31  
PRIOR APPLICATION NUMBER: 60/180,628  
PRIOR FILING DATE: 2000-02-04  
PRIOR APPLICATION NUMBER: 60/231,968  
PRIOR FILING DATE: 2000-09-12  
NUMBER OF SEQ ID NOS: 97  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 83  
LENGTH: 150  
TYPE: PRT  
ORGANISM: Homo sapiens  
J9-915-582-83

Query Match 39.0%; Score 48; DB 9; Length 150;  
Best Local Similarity 75.0%; Pred. No. 46;  
Matches 6; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

QY 2 NWRCCCLIP 9  
DB 125 NWKCCFIP 132

RESULT 11  
US-09-833-129-49  
Sequence 49, Application US/09832129  
Publication No. US20030027297A1  
GENERAL INFORMATION:  
APPLICANT: Fiscella et al.  
TITLE OF INVENTION: 19 Human secreted proteins  
FILE REFERENCE: P2045PI  
CURRENT APPLICATION NUMBER: US/09/832,129  
CURRENT FILING DATE: 2001-04-11  
PRIOR APPLICATION NUMBER: PCT/US00/28664  
PRIOR FILING DATE: 2000-10-17  
PRIOR APPLICATION NUMBER: 60/163,085  
PRIOR FILING DATE: 1999-11-02  
PRIOR APPLICATION NUMBER: 60/172,411  
PRIOR FILING DATE: 1999-12-17  
NUMBER OF SEQ ID NOS: 70  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 49  
LENGTH: 150  
TYPE: PRT  
ORGANISM: Homo sapiens  
09-832-129-49

Query Match 39.0%; Score 48; DB 10; Length 150;  
Best Local Similarity 75.0%; Pred. No. 46;  
Matches 6; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

QY 2 NWRCCCLIP 9  
DB 125 NWKCCFIP 132

ULT 12  
09-833-245-1472  
Sequence 1472, Application US/09833245  
Publication No. US20040010134A1  
GENERAL INFORMATION:  
APPLICANT: Human Genome Sciences, Inc.  
TITLE OF INVENTION: Albumin Fusion Proteins  
FILE REFERENCE: PF546PCT  
CURRENT APPLICATION NUMBER: US/09/833,245  
CURRENT FILING DATE: 2001-04-12  
NUMBER OF SEQ ID NOS: 2267  
SOFTWARE: PatentIn Ver. 2.1

TITLE OF INVENTION: 17 Human Secreted Proteins  
FILE REFERENCE: PS723PI  
CURRENT APPLICATION NUMBER: US/09/915,582  
CURRENT FILING DATE: 2001-07-27  
PRIOR APPLICATION NUMBER: PCT/US01/01431  
PRIOR FILING DATE: 2001-01-17  
PRIOR APPLICATION NUMBER: 60/179,065  
PRIOR FILING DATE: 2000-01-31  
PRIOR APPLICATION NUMBER: 60/180,628  
PRIOR FILING DATE: 2000-02-04  
PRIOR APPLICATION NUMBER: 60/231,968  
PRIOR FILING DATE: 2000-09-12  
NUMBER OF SEQ ID NOS: 97  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 83  
LENGTH: 150  
TYPE: PRT  
ORGANISM: Homo sapiens  
J9-915-582-83

Query Match 39.0%; Score 48; DB 11; Length 150;  
Best Local Similarity 75.0%; Pred. No. 46;  
Matches 6; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

QY 2 NWRCCCLIP 9  
DB 125 NWKCCFIP 132

RESULT 13  
US-09-833-245-1473  
Sequence 1473, Application US/09833245  
Publication No. US20040010134A1  
GENERAL INFORMATION:  
APPLICANT: Human Genome Sciences, Inc.  
TITLE OF INVENTION: Albumin Fusion Proteins  
FILE REFERENCE: PF546PCT  
CURRENT APPLICATION NUMBER: US/09/833,245  
CURRENT FILING DATE: 2001-04-12  
PRIOR APPLICATION NUMBER: 60/229,358  
PRIOR FILING DATE: 2000-04-12  
PRIOR APPLICATION NUMBER: 60/256,931  
PRIOR FILING DATE: 2000-12-21  
PRIOR APPLICATION NUMBER: 60/199,384  
PRIOR FILING DATE: 2000-04-25  
NUMBER OF SEQ ID NOS: 2267  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 1473  
LENGTH: 150  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-833-245-1473

Query Match 39.0%; Score 48; DB 11; Length 150;  
Best Local Similarity 75.0%; Pred. No. 46;  
Matches 6; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

QY 2 NWRCCCLIP 9  
DB 125 NWKCCFIP 132

RESULT 14  
US-09-833-245-2227  
Sequence 2227, Application US/09833245  
Publication No. US20040010134A1  
GENERAL INFORMATION:  
APPLICANT: Human Genome Sciences, Inc.  
TITLE OF INVENTION: Albumin Fusion Proteins  
FILE REFERENCE: PF546PCT  
CURRENT APPLICATION NUMBER: US/09/833,245  
CURRENT FILING DATE: 2001-04-12  
PRIOR APPLICATION NUMBER: 60/229,358  
PRIOR FILING DATE: 2000-04-12  
PRIOR APPLICATION NUMBER: 60/256,931  
PRIOR FILING DATE: 2000-12-21  
PRIOR APPLICATION NUMBER: 60/199,384  
PRIOR FILING DATE: 2000-04-25  
NUMBER OF SEQ ID NOS: 2267  
SOFTWARE: PatentIn Ver. 2.1

3Q ID NO 2227  
LENGTH: 150  
TYPE: PRT  
ORGANISM: Homo sapiens  
09-833-245-2227  
  
Query Match 39.0%; Score 48; DB 11; Length 150;  
Best Local Similarity 75.0%; Pred. No. 46;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
2 NWRCCCLIP 9  
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125 NWKCCFIP 132

RESULT 15  
US-10-704-182  
Sequence 83, Application US/10050704  
Publication No. US20030050442A1  
GENERAL INFORMATION:  
APPLICANT: Ruben et al.  
TITLE OF INVENTION: 62 Human Secreted Proteins  
FILE REFERENCE: P2039P1  
CURRENT APPLICATION NUMBER: US/10/050,704  
CURRENT FILING DATE: 2002-01-18  
PRIOR APPLICATION NUMBER: 09/684,524  
PRIOR FILING DATE: 2000-10-10  
PRIOR APPLICATION NUMBER: PCT/US00/08979  
PRIOR FILING DATE: 2000-04-06  
PRIOR APPLICATION NUMBER: 60/128,693  
PRIOR FILING DATE: 1999-04-09  
PRIOR APPLICATION NUMBER: 60/130,991  
PRIOR FILING DATE: 1999-04-26  
NUMBER OF SEQ ID NOS: 344  
SOFTWARE: PatentIn Ver. 2.0  
EQ ID NO 182  
LENGTH: 150  
TYPE: PRT  
ORGANISM: Homo sapiens  
10-050-704-182

Query Match 39.0%; Score 48; DB 14; Length 150;  
Best Local Similarity 75.0%; Pred. No. 46;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
2 NWRCCCLIP 9  
||:||||  
125 NWKCCFIP 132

ULT 16  
10-277-802-63  
Sequence 63, Application US/10277802  
Publication No. US20030190707A1  
GENERAL INFORMATION:  
APPLICANT: Rosen et al.  
TITLE OF INVENTION: 17 Human Secreted Proteins  
FILE REFERENCE: PS723P1  
CURRENT APPLICATION NUMBER: US/10/277,802  
CURRENT FILING DATE: 2002-10-23  
PRIOR APPLICATION NUMBER: 09/915,582  
PRIOR FILING DATE: 2001-07-27  
PRIOR APPLICATION NUMBER: PCT/US01/01431  
PRIOR FILING DATE: 2001-01-17  
PRIOR APPLICATION NUMBER: 60/179,065  
PRIOR FILING DATE: 2000-01-31  
PRIOR APPLICATION NUMBER: 60/180,628  
PRIOR FILING DATE: 2000-02-04  
PRIOR APPLICATION NUMBER: 60/231,968  
PRIOR FILING DATE: 2000-09-12  
NUMBER OF SEQ ID NOS: 97  
SOFTWARE: PatentIn Ver. 2.0  
EQ ID NO 63

3Q ID NO 2227  
LENGTH: 150  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-277-802-63  
  
Query Match 39.0%; Score 48; DB 14; Length 150;  
Best Local Similarity 75.0%; Pred. No. 46;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
2 NWRCCCLIP 9  
||:||||  
125 NWKCCFIP 132

RESULT 17  
US-10-277-802-83  
Sequence 83, Application US/10277802  
Publication No. US20030190707A1  
GENERAL INFORMATION:  
APPLICANT: Rosen et al.  
TITLE OF INVENTION: 17 Human Secreted Proteins  
FILE REFERENCE: PS723P1  
CURRENT APPLICATION NUMBER: US/10/277,802  
CURRENT FILING DATE: 2002-10-23  
PRIOR APPLICATION NUMBER: 09/915,582  
PRIOR FILING DATE: 2001-07-27  
PRIOR APPLICATION NUMBER: PCT/US01/01431  
PRIOR FILING DATE: 2001-01-17  
PRIOR APPLICATION NUMBER: 60/179,065  
PRIOR FILING DATE: 2000-01-31  
PRIOR APPLICATION NUMBER: 60/180,628  
PRIOR FILING DATE: 2000-02-04  
PRIOR APPLICATION NUMBER: 60/231,968  
PRIOR FILING DATE: 2000-09-12  
NUMBER OF SEQ ID NOS: 97  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 83  
LENGTH: 150  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-277-802-83

Query Match 39.0%; Score 48; DB 14; Length 150;  
Best Local Similarity 75.0%; Pred. No. 46;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
2 NWRCCCLIP 9  
||:||||  
125 NWKCCFIP 132

RESULT 18  
US-09-832-129-64  
Sequence 64, Application US/09832129  
Publication No. US20030027297A1  
GENERAL INFORMATION:  
APPLICANT: Fiscella et al.  
TITLE OF INVENTION: 19 Human secreted proteins  
FILE REFERENCE: P2045P1  
CURRENT APPLICATION NUMBER: US/09/832,129  
CURRENT FILING DATE: 2001-04-11  
PRIOR APPLICATION NUMBER: PCT/US00/28664  
PRIOR FILING DATE: 2000-10-17  
PRIOR APPLICATION NUMBER: 60/163,085  
PRIOR FILING DATE: 1999-11-02  
PRIOR APPLICATION NUMBER: 60/172,411  
PRIOR FILING DATE: 1999-12-17  
NUMBER OF SEQ ID NOS: 70  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 64  
LENGTH: 192  
TYPE: PRT  
ORGANISM: Homo sapiens

09-832-129-64  
Query Match 39.0%; Score 48; DB 10; Length 192;  
Best Local Similarity 75.0%; Pred. No. 56;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

2 NWRCClip 9  
||:||||  
167 NWKCCFIP 174

ULT 19  
10-205-823-158  
Sequence 158, Application US/10205823  
Publication No. US20030108963A1  
GENERAL INFORMATION:  
APPLICANT: Schlegel, Robert  
APPLICANT: Monahan, John E.  
APPLICANT: Endege, Wilson O.  
APPLICANT: Gannavarapu, Manjula  
APPLICANT: Gorbatscheva, Bella  
APPLICANT: Hoersch, Sebastian  
APPLICANT: Kamatkar, Shubhangi  
APPLICANT: Womsey, Angela M.  
APPLICANT: Glatt, Karen  
APPLICANT: Zhao, Xumei  
APPLICANT: Anderson, Dustin  
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND  
METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND  
THERAPY OF PROSTATE CANCER  
FILE REFERENCE: WRI-044  
CURRENT APPLICATION NUMBER: US/10/205,823  
CURRENT FILING DATE: 2002-07-25  
PRIOR APPLICATION NUMBER: 60/307,982  
PRIOR FILING DATE: 2001-07-25  
PRIOR APPLICATION NUMBER: 60/314,356  
PRIOR FILING DATE: 2001-06-22  
PRIOR APPLICATION NUMBER: 60/325,020  
PRIOR FILING DATE: 2001-09-25  
PRIOR APPLICATION NUMBER: 60/341,746  
PRIOR FILING DATE: 2001-12-12  
PRIOR APPLICATION NUMBER: 60/362,158  
PRIOR FILING DATE: 2002-03-05  
NUMBER OF SEQ ID NOS: 455  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 158  
LENGTH: 338  
TYPE: PRT  
ORGANISM: Homo sapiens  
10-205-823-158

Query Match 39.0%; Score 48; DB 14; Length 338;  
Best Local Similarity 75.0%; Pred. No. 90;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

2 NWRCClip 9  
||:||||  
313 NWKCCFIP 320

ULT 20  
10-225-567A-601  
Sequence 601, Application US/10225567A  
Publication No. US20030113798A1  
GENERAL INFORMATION:  
APPLICANT: LifeSpan Biosciences  
APPLICANT: Brown, Joseph P.  
APPLICANT: Burner, Glenna C.  
APPLICANT: Roush, Christine L.  
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS  
FILE REFERENCE: 1920-4-4  
CURRENT APPLICATION NUMBER: US/10/225,567A  
CURRENT FILING DATE: 2001-12-19

PRIOR APPLICATION NUMBER: 60/257,144  
PRIOR FILING DATE: 2000-12-19  
NUMBER OF SEQ ID NOS: 2292  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 601  
LENGTH: 338  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-225-567A-601

Query Match 39.0%; Score 48; DB 14; Length 338;  
Best Local Similarity 75.0%; Pred. No. 90;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 NWRCClip 9  
||:||||  
Db 313 NWKCCFIP 320

RESULT 21  
US-10-295-027-774  
Sequence 774, Application US/10295027  
Publication No. US20030232350A1  
GENERAL INFORMATION:  
APPLICANT: Afar, Daniel  
APPLICANT: Aziz, Natasha  
APPLICANT: Ginsberg, Wendy M.  
APPLICANT: Gish, Kurt C.  
APPLICANT: Glynn, Richard  
APPLICANT: Hevizi, Peter A.  
APPLICANT: Mack, David H.  
APPLICANT: Murray, Richard  
APPLICANT: Watson, Susan R.  
APPLICANT: Eos Biotechnology, Inc.  
TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and  
Methods of Screening for Modulators of Cancer  
FILE REFERENCE: 018501-012500US  
CURRENT APPLICATION NUMBER: US/10/295,027  
CURRENT FILING DATE: 2002-11-13  
PRIOR APPLICATION NUMBER: US 09/663,733  
PRIOR FILING DATE: 2000-09-15  
PRIOR APPLICATION NUMBER: US 60/350,666  
PRIOR FILING DATE: 2001-11-13  
PRIOR APPLICATION NUMBER: US 60/335,394  
PRIOR FILING DATE: 2001-11-15  
PRIOR APPLICATION NUMBER: US 60/332,464  
PRIOR FILING DATE: 2001-11-21  
PRIOR APPLICATION NUMBER: US 60/334,393  
PRIOR FILING DATE: 2001-11-29  
PRIOR APPLICATION NUMBER: US 60/340,376  
PRIOR FILING DATE: 2001-12-14  
PRIOR APPLICATION NUMBER: US 60/347,211  
PRIOR FILING DATE: 2002-01-08  
PRIOR APPLICATION NUMBER: US 60/347,349  
PRIOR FILING DATE: 2002-01-10  
PRIOR APPLICATION NUMBER: US 60/355,250  
PRIOR FILING DATE: 2002-02-08  
PRIOR APPLICATION NUMBER: US 60/356,714  
PRIOR FILING DATE: 2002-02-13  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 1386  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 774  
LENGTH: 338  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-295-027-774

Query Match 39.0%; Score 48; DB 15; Length 338;  
Best Local Similarity 75.0%; Pred. No. 90;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 NWRCClip 9

|||||  
313 NWKCCFIP 320

UT 22  
10-295-027-1202  
sequence 1202, Application US/10295027  
ublication No. US20030232350A1  
GENERAL INFORMATION:  
APPLICANT: Afar, Daniel  
APPLICANT: Aziz, Natasha  
APPLICANT: Ginsberg, Wendy M.  
APPLICANT: Gish, Kurt C.  
APPLICANT: Glynn, Richard  
APPLICANT: Hevezi, Peter A.  
APPLICANT: Mack, David H.  
APPLICANT: Murray, Richard  
APPLICANT: Watson, Susan R.  
APPLICANT: Eos Biotechnology, Inc.  
TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and  
TITLE OF INVENTION: Methods of Screening for Modulators of Cancer  
FILE REFERENCE: 018501-012500US  
CURRENT APPLICATION NUMBER: US/10/295,027  
CURRENT FILING DATE: 2002-11-13  
PRIOR APPLICATION NUMBER: US 09/663,733  
PRIOR FILING DATE: 2000-09-15  
PRIOR APPLICATION NUMBER: US 60/350,666  
PRIOR FILING DATE: 2001-11-13  
PRIOR APPLICATION NUMBER: US 60/335,394  
PRIOR FILING DATE: 2001-11-15  
PRIOR APPLICATION NUMBER: US 60/332,464  
PRIOR FILING DATE: 2001-11-21  
PRIOR APPLICATION NUMBER: US 60/334,393  
PRIOR FILING DATE: 2001-11-29  
PRIOR APPLICATION NUMBER: US 60/340,376  
PRIOR FILING DATE: 2001-12-14  
PRIOR APPLICATION NUMBER: US 60/347,211  
PRIOR FILING DATE: 2002-01-08  
PRIOR APPLICATION NUMBER: US 60/347,349  
PRIOR FILING DATE: 2002-01-10  
PRIOR APPLICATION NUMBER: US 60/355,250  
PRIOR FILING DATE: 2002-02-08  
PRIOR APPLICATION NUMBER: US 60/356,714  
PRIOR FILING DATE: 2002-02-13  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 1386  
SOFTWARE: PatentIn Ver. 2.1  
EQ ID NO 1202  
LENGTH: 338  
TYPE: PRT  
ORGANISM: Homo sapiens  
10-295-027-1202

Query Match 39.0%; Score 48; DB 15; Length 338;  
est Local Similarity 75.0%; Pred. No. 90;  
atches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
2 NWKCCFIP 9  
|||||  
313 NWKCCFIP 320

UT 23  
09-923-301-981  
sequence 981, Application US/09925301  
atent No. US2002052308A1  
GENERAL INFORMATION:  
APPLICANT: Rosen et al.  
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
FILE REFERENCE: P8106  
CURRENT APPLICATION NUMBER: US/09/925,301  
CURRENT FILING DATE: 2001-08-10  
PRIOR APPLICATION NUMBER: PCT/US00/05882

; PRIOR FILING DATE: 2000-03-08  
; PRIOR APPLICATION NUMBER: 60/124,270  
; PRIOR FILING DATE: 1999-03-12  
; NUMBER OF SEQ ID NOS: 1694  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 981  
; LENGTH: 343  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (343)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
US-09-925-301-981

Query Match 39.0%; Score 48; DB 9; Length 343;  
Best Local Similarity 75.0%; Pred. No. 91;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 NWKCCFIP 9  
|||||  
Db 318 NWKCCFIP 325

RESULT 24  
US-09-897-465-10  
; Sequence 10, Application US/09897465  
; Patent No. US2002022715A1  
; GENERAL INFORMATION:  
; APPLICANT: Olivera, Baldomero M.  
; APPLICANT: McIntosh, J. Michael  
; APPLICANT: Yoshikami, Doju  
; APPLICANT: Cartier, G. Edward  
; APPLICANT: Luo, Siqin  
; APPLICANT: University of Utah Research Foundation  
; TITLE OF INVENTION: Uses of Alpha-Conotoxin Peptides  
; FILE REFERENCE: Uses of Alpha-Conotoxins  
; CURRENT APPLICATION NUMBER: US/09/897,465  
; CURRENT FILING DATE: 2001-07-03  
; PRIOR APPLICATION NUMBER: US 60/080,588  
; PRIOR FILING DATE: 1998-04-03  
; PRIOR APPLICATION NUMBER: US 60/070,153  
; PRIOR FILING DATE: 1997-12-31  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 10  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:ALOL derivative  
; OTHER INFORMATION: of C. purpurascens Pnia  
US-09-897-465-10

Query Match 38.2%; Score 47; DB 9; Length 16;  
Best Local Similarity 40.0%; Pred. No. 9.7;  
Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;  
5 CCLIPACRRNHKKFC 19  
|||||  
2 CCSLPPCALNPDYC 16

RESULT 25  
US-10-072-602B-598  
; Sequence 598, Application US/10072602B  
; Publication No. US20030109670A1  
; GENERAL INFORMATION:  
; APPLICANT: University of Utah Research Foundation  
; APPLICANT: Cognetix, Inc.  
; APPLICANT: Olivera, Baldomero M.  
; APPLICANT: McIntosh, J. Michael  
; APPLICANT: Watkins, Maren



APPLICANT: Garrett, James E.  
 APPLICANT: Cruz, Lourdes J.  
 APPLICANT: Grilley, Michelle  
 APPLICANT: Schoenfeld, Robert M.  
 APPLICANT: Walker, Craig  
 APPLICANT: Shetty, Reshma  
 APPLICANT: Jones, Robert M.  
 TITLE OF INVENTION: Cone Snail Peptides  
 FILE REFERENCE: 2314-249  
 CURRENT APPLICATION NUMBER: US/10/072,602B  
 CURRENT FILING DATE: 2002-02-11  
 PRIOR APPLICATION NUMBER: US 60/267,408  
 PRIOR FILING DATE: 2001-02-09  
 NUMBER OF SEQ ID NOS: 638  
 SOFTWARE: PatentIn version 3.0  
 SEQ ID NO 598  
 LENGTH: 22  
 TYPE: PRT  
 ORGANISM: Conus arenatus  
 10-072-602B-598

Query Match 38.2%; Score 47; DB 14; Length 22;  
 Best Local Similarity 46.7%; Pred. No. 13;  
 Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;  
 5 CCLIPACRRNHKKFC 19  
 |||||:|:|  
 4 CCTIPSCWDYKERC 18

ULT 26  
 10-072-602B-599  
 Sequence 599, Application US/10072602B  
 Publication No. US20030109670A1  
 GENERAL INFORMATION:  
 APPLICANT: University of Utah Research Foundation  
 APPLICANT: Cognetix, Inc.  
 APPLICANT: Olivera, Baldomero M.  
 APPLICANT: McIntosh, J. Michael  
 APPLICANT: Watkins, Maren  
 APPLICANT: Garrett, James E.  
 APPLICANT: Cruz, Lourdes J.  
 APPLICANT: Grilley, Michelle  
 APPLICANT: Schoenfeld, Robert M.  
 APPLICANT: Walker, Craig  
 APPLICANT: Shetty, Reshma  
 APPLICANT: Jones, Robert M.  
 TITLE OF INVENTION: Cone Snail Peptides  
 FILE REFERENCE: 2314-249  
 CURRENT APPLICATION NUMBER: US/10/072,602B  
 CURRENT FILING DATE: 2002-02-11  
 PRIOR APPLICATION NUMBER: US 60/267,408  
 PRIOR FILING DATE: 2001-02-09  
 NUMBER OF SEQ ID NOS: 638  
 SOFTWARE: PatentIn version 3.0  
 SEQ ID NO 599  
 LENGTH: 22  
 TYPE: PRT  
 ORGANISM: Conus eburneus  
 10-072-602B-599

Query Match 38.2%; Score 47; DB 14; Length 22;  
 Best Local Similarity 46.7%; Pred. No. 13;  
 Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;  
 5 CCLIPACRRNHKKFC 19  
 |||||:|:|  
 4 CCTIPSCWDYKERC 18

ULT 27  
 10-072-602B-392  
 Sequence 392, Application US/10072602B

Publication No. US20030109670A1  
 GENERAL INFORMATION:  
 APPLICANT: University of Utah Research Foundation  
 APPLICANT: Cognetix, Inc.  
 APPLICANT: Olivera, Baldomero M.  
 APPLICANT: McIntosh, J. Michael  
 APPLICANT: Watkins, Maren  
 APPLICANT: Garrett, James E.  
 APPLICANT: Cruz, Lourdes J.  
 APPLICANT: Grilley, Michelle  
 APPLICANT: Schoenfeld, Robert M.  
 APPLICANT: Walker, Craig  
 APPLICANT: Shetty, Reshma  
 APPLICANT: Jones, Robert M.  
 TITLE OF INVENTION: Cone Snail Peptides  
 FILE REFERENCE: 2314-249  
 CURRENT APPLICATION NUMBER: US/10/072,602B  
 CURRENT FILING DATE: 2002-02-11  
 PRIOR APPLICATION NUMBER: US 60/267,408  
 PRIOR FILING DATE: 2001-02-09  
 NUMBER OF SEQ ID NOS: 638  
 SOFTWARE: PatentIn version 3.0  
 SEQ ID NO 392  
 LENGTH: 63  
 TYPE: PRT  
 ORGANISM: Conus arenatus  
 US-10-072-602B-392

Query Match 38.2%; Score 47; DB 14; Length 63;  
 Best Local Similarity 46.7%; Pred. No. 30;  
 Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;  
 QY 5 CCLIPACRRNHKKFC 19  
 |||||:|:|  
 Db 45 CCTIPSCWDYKERC 59

RESULT 28  
 US-10-072-602B-395  
 Sequence 395, Application US/10072602B  
 Publication No. US20030109670A1  
 GENERAL INFORMATION:  
 APPLICANT: University of Utah Research Foundation  
 APPLICANT: Cognetix, Inc.  
 APPLICANT: Olivera, Baldomero M.  
 APPLICANT: McIntosh, J. Michael  
 APPLICANT: Watkins, Maren  
 APPLICANT: Garrett, James E.  
 APPLICANT: Cruz, Lourdes J.  
 APPLICANT: Grilley, Michelle  
 APPLICANT: Schoenfeld, Robert M.  
 APPLICANT: Walker, Craig  
 APPLICANT: Shetty, Reshma  
 APPLICANT: Jones, Robert M.  
 TITLE OF INVENTION: Cone Snail Peptides  
 FILE REFERENCE: 2314-249  
 CURRENT APPLICATION NUMBER: US/10/072,602B  
 CURRENT FILING DATE: 2002-02-11  
 PRIOR APPLICATION NUMBER: US 60/267,408  
 PRIOR FILING DATE: 2001-02-09  
 NUMBER OF SEQ ID NOS: 638  
 SOFTWARE: PatentIn version 3.0  
 SEQ ID NO 395  
 LENGTH: 63  
 TYPE: PRT  
 ORGANISM: Conus eburneus  
 US-10-072-602B-395

Query Match 38.2%; Score 47; DB 14; Length 63;  
 Best Local Similarity 46.7%; Pred. No. 30;  
 Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;  
 QY 5 CCLIPACRRNHKKFC 19

|||||:|:|:|  
45 CCTPSCWDYKERC 59

LT 29  
0-097-340-111  
Sequence 111, Application US/10097340  
Publication No. US20030087250A1  
GENERAL INFORMATION:  
APPLICANT: John MONAHAN  
APPLICANT: Manjula GANNAVAPU  
APPLICANT: Sebastian HOERSCH  
APPLICANT: Shubhangi KAMATKAR  
APPLICANT: Steve G. KOVATS  
APPLICANT: Rachel E. MEYERS  
APPLICANT: Michael MORRISSEY  
APPLICANT: Peter OLANDT  
APPLICANT: Ami SEN  
APPLICANT: Peter VEIBY  
APPLICANT: Gordon B. MILLS  
APPLICANT: Robert C. BAST, Jr.  
APPLICANT: Karen LU  
APPLICANT: Rosemarie SCHMANDT  
APPLICANT: Xumei ZHAO  
APPLICANT: Karen GLATT  
TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,  
Assessment, Prevention, and Therapy of Ovarian Cancer  
FILE REFERENCE: MRI-030  
CURRENT APPLICATION NUMBER: US/10/097,340  
CURRENT FILING DATE: 2002-03-14  
PRIOR APPLICATION NUMBER: 60/276,025  
PRIOR FILING DATE: 2001-03-14  
PRIOR APPLICATION NUMBER: 60/325,149  
PRIOR FILING DATE: 2001-09-26  
PRIOR APPLICATION NUMBER: 60/276,026  
PRIOR FILING DATE: 2001-03-14  
PRIOR APPLICATION NUMBER: 60/324,967  
PRIOR FILING DATE: 2001/09/26  
PRIOR APPLICATION NUMBER: 60/311,732  
PRIOR FILING DATE: 2001-08-10  
PRIOR APPLICATION NUMBER: 60/325,102  
PRIOR FILING DATE: 2001-09-26  
PRIOR APPLICATION NUMBER: 60/323,580  
PRIOR FILING DATE: 2001-09-19  
NUMBER OF SEQ ID NOS: 363  
SOFTWARE: Fast-SEQ for Windows Version 4.0  
SEQ ID NO 111  
LENGTH: 257  
TYPE: PRT  
ORGANISM: Homo sapiens  
10-097-340-111

Query Match 38.2%; Score 47; DB 14; Length 257;  
Best Local Similarity 50.0%; Pred. No. 97;  
Matches 8; Conservative 3; Mismatches 3; Indels 2; Gaps 1;

|||||:|:|:|  
1 FNRCC--LIPACRN 14  
84 FNNHCGEMAPACKRH 99

ULT 30  
10-264-049-2498  
Sequence 2498, Application US/10264049  
Publication No. US20040005579A1  
GENERAL INFORMATION:  
APPLICANT: Birse et al.  
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
FILE REFERENCE: PA133P1  
CURRENT APPLICATION NUMBER: US/10/264,049  
CURRENT FILING DATE: 2002-10-04  
PRIOR APPLICATION NUMBER: PCT/US01/18569  
PRIOR FILING DATE: 2001-06-07

;; PRIOR APPLICATION NUMBER: US 60/209,467  
;; PRIOR FILING DATE: 2000-06-07  
;; NUMBER OF SEQ ID NOS: 4360  
;; SOFTWARE: PatentIn Ver. 3.1  
;; SEQ ID NO 2498  
;; LENGTH: 270  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-10-264-049-2498

Query Match 38.2%; Score 47; DB 15; Length 270;  
Best Local Similarity 50.0%; Pred. No. 1e+02;  
Matches 8; Conservative 3; Mismatches 2; Indels 2; Gaps 1;

QY 1 FNRCC--LIPACRN 14  
|||:|:|:|  
DB 97 FNNHCGEMAPACKRH 112

RESULT 31  
US-09-205-658-152  
; Sequence 152, Application US/09205658  
; Patent No. US20010029617A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruvkun, Gary  
; APPLICANT: Ogg, Scott  
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR  
; FILE REFERENCE: 00786/351004  
; CURRENT APPLICATION NUMBER: US/09/205,658  
; CURRENT FILING DATE: 1998-12-03  
; EARLIER APPLICATION NUMBER: 08/857,076  
; EARLIER FILING DATE: 1997-05-15  
; EARLIER APPLICATION NUMBER: 08/888,534  
; EARLIER FILING DATE: 1997-07-07  
; EARLIER APPLICATION NUMBER: US98/10080  
; EARLIER FILING DATE: 1998-05-15  
; NUMBER OF SEQ ID NOS: 328  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 152  
; LENGTH: 46  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: (1)...(46)  
; OTHER INFORMATION: Xaa = Any Amino Acid  
US-09-205-658-152

Query Match 37.4%; Score 46; DB 9; Length 46;  
Best Local Similarity 43.8%; Pred. No. 32;  
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 4 RCCLIPACRNHHKFC 19  
|||:|:|:|:|:|:|  
DB 31 KCCLIGCTKRSIAKVC 46

RESULT 32  
US-09-963-693-152  
; Sequence 152, Application US/09963693  
; Publication No. US20030181364A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruvkun, Gary  
; APPLICANT: Ogg, Scott  
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR  
; FILE REFERENCE: 00786/351004  
; CURRENT APPLICATION NUMBER: US/09/963,693  
; CURRENT FILING DATE: 2001-09-25  
; PRIOR APPLICATION NUMBER: US/09/205,658  
; PRIOR FILING DATE: 1998-12-03  
; PRIOR APPLICATION NUMBER: 08/857,076

PRIOR FILING DATE: 1997-05-15  
PRIOR APPLICATION NUMBER: 08/888,534  
PRIOR FILING DATE: 1997-07-07  
PRIOR APPLICATION NUMBER: US98/10080  
PRIOR FILING DATE: 1998-05-15  
NUMBER OF SEQ ID NOS: 328  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 152  
LENGTH: 46  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: VARIANT  
LOCATION: (1)...(46)  
OTHER INFORMATION: Xaa = Any Amino Acid  
19-963-693-152

Query Match 37.4%; Score 46; DB 10; Length 46;  
Best Local Similarity 43.8%; Pred. No. 32;  
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

JLT 33  
10-072-602B-428  
Sequence 428, Application US/10072602B  
Publication No. US20030109670A1  
GENERAL INFORMATION:  
APPLICANT: University of Utah Research Foundation  
APPLICANT: Cognetix, Inc.  
APPLICANT: Olivera, Baldomero M.  
APPLICANT: McIntosh, J. Michael  
APPLICANT: Watkins, Maren  
APPLICANT: Garrett, James E.  
APPLICANT: Cruz, Lourdes J.  
APPLICANT: Grilley, Michelle  
APPLICANT: Schoenfeld, Robert M.  
APPLICANT: Walker, Craig  
APPLICANT: Shetty, Reshma  
APPLICANT: Jones, Robert M.  
TITLE OF INVENTION: Cone Snail Peptides  
FILE REFERENCE: 2314-249  
CURRENT APPLICATION NUMBER: US/10/072,602B  
CURRENT FILING DATE: 2002-02-11  
PRIOR APPLICATION NUMBER: US 60/267,408  
PRIOR FILING DATE: 2001-02-09  
NUMBER OF SEQ ID NOS: 638  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 428  
LENGTH: 57  
TYPE: PRT  
ORGANISM: Conus leopardus  
10-072-602B-428

Query Match 37.4%; Score 46; DB 14; Length 57;  
Best Local Similarity 43.8%; Pred. No. 38;  
Matches 7; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

JULT 34  
09-908-741-89  
Sequence 89, Application US/09908741  
Publication No. US20030050435A1  
GENERAL INFORMATION:  
APPLICANT: Olivera, Baldomero M.  
APPLICANT: Layer, Richard T.

APPLICANT: Watkins, Maren  
APPLICANT: Hillyard, David R.  
APPLICANT: McIntosh, J. Michael  
APPLICANT: Schoenfeld, Robert  
APPLICANT: Jones, Robert M.  
APPLICANT: Nielsen, Jake  
APPLICANT: University of Utah Research Foundation  
APPLICANT: Cognetix, Inc.  
TITLE OF INVENTION: Alpha Conotoxin Peptides  
FILE REFERENCE: Alpha CIP  
CURRENT APPLICATION NUMBER: US/09/908,741  
CURRENT FILING DATE: 2001-07-20  
PRIOR APPLICATION NUMBER: US 60/116,891  
PRIOR FILING DATE: 1999-01-22  
PRIOR APPLICATION NUMBER: US 60/116,882  
PRIOR FILING DATE: 1999-01-22  
PRIOR APPLICATION NUMBER: US 09/488,799  
PRIOR FILING DATE: 2000-01-21  
PRIOR APPLICATION NUMBER: US 60/219,407  
PRIOR FILING DATE: 2000-07-20  
PRIOR APPLICATION NUMBER: US 60/221,557  
PRIOR FILING DATE: 2000-07-28  
NUMBER OF SEQ ID NOS: 125  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 89  
LENGTH: 62  
TYPE: PRT  
ORGANISM: Conus ermineus  
US-09-908-741-89

Query Match 37.4%; Score 46; DB 10; Length 62;  
Best Local Similarity 46.7%; Pred. No. 41;  
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 5 CCLIPACRRNHKKFC 19  
DB 47 CCSPACRVNPPQIC 61

RESULT 35  
US-10-205-823-349  
Sequence 349, Application US/10205823  
Publication No. US20030108963A1  
GENERAL INFORMATION:  
APPLICANT: Schlegel, Robert  
APPLICANT: Monahan, John E.  
APPLICANT: Endege, Wilson O.  
APPLICANT: Gannavarapu, Manjula  
APPLICANT: Gorbacheva, Bella  
APPLICANT: Hoersch, Sebastian  
APPLICANT: Kamatkar, Shubhangi  
APPLICANT: Womsey, Angela M.  
APPLICANT: Glatt, Karen  
APPLICANT: Zhao, Xumei  
APPLICANT: Anderson, Dustin  
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND  
METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND  
THERAPY OF PROSTATE CANCER  
FILE REFERENCE: MRI-044  
CURRENT APPLICATION NUMBER: US/10/205,823  
CURRENT FILING DATE: 2002-07-25  
PRIOR APPLICATION NUMBER: 60/307,982  
PRIOR FILING DATE: 2001-07-25  
PRIOR APPLICATION NUMBER: 60/314,356  
PRIOR FILING DATE: 2001-08-22  
PRIOR APPLICATION NUMBER: 60/325,020  
PRIOR FILING DATE: 2001-09-25  
PRIOR APPLICATION NUMBER: 60/341,746  
PRIOR FILING DATE: 2001-12-12  
PRIOR APPLICATION NUMBER: 60/362,158  
NUMBER OF SEQ ID NOS: 455  
SOFTWARE: FastSeq for Windows Version 4.0

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EQ ID NO 349
LENGTH: 185
TYPE: PRT
ORGANISM: Homo sapiens
10-205-823-349

Very Match      37.4%; Score 46; DB 14; Length 185;
1st Local Similarity 43.8%; Pred. NO. 1e+02;
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

      4 RCCLIPACRRNHKKFC 19
      :|||:|:|:|:|:|:|
      170 KCCLIGTKKSLAKYC 185

rch completed: February 18, 2004, 06:26:26
time : 610 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

protein - protein search, using sw model

on: February 18, 2004, 06:03:18 : Search time 42 Seconds  
(without alignments)  
23.355 Million cell updates/sec

US-09-806-376-1

ect score: 123

ence: 1 FNRCLIPACRNHKFC 19

ing table: BLOSUM62

Gapop 10.0 , Gapext 0.5

ched: 389414 seqs, 51625971 residues

al number of hits satisfying chosen parameters: 389414

umum DB seq length: 0

umum DB seq length: 2000000000

:-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

abase : Issued Patents:AA\*

1: /cgn2\_6/prodata/2/iaa/5A-COMB.pep:\*

2: /cgn2\_6/prodata/2/iaa/5B-COMB.pep:\*

3: /cgn2\_6/prodata/2/iaa/5A-COMB.pep:\*

4: /cgn2\_6/prodata/2/iaa/6B-COMB.pep:\*

5: /cgn2\_6/prodata/2/iaa/PCITS-COMB.pep:\*

6: /cgn2\_6/prodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Alt No.	Score	Query Match	Length	DB ID	Description
1	50	40.7	70	1	US-08-137-800-49
2	50	40.7	70	1	US-08-477-383-49
3	50	40.7	70	1	US-08-487-174-49
4	50	40.7	70	1	US-08-480-750-49
5	50	40.7	398	4	US-09-252-991A-26217
6	49	39.8	101	4	US-08-252-991A-20226
7	48	39.0	16	3	US-09-219-446B-9
8	48	39.0	226	4	US-09-252-991A-23844
9	48	39.0	234	4	US-09-270-391-16
10	47	38.2	16	3	US-09-219-446B-10
11	46	37.4	18	1	US-08-137-800-32
12	46	37.4	18	1	US-08-477-383-32
13	46	37.4	18	1	US-08-487-174-32
14	46	37.4	18	1	US-08-480-750-32
15	46	37.4	24	6	5464756-3
16	46	37.4	62	3	US-09-488-799-89
17	46	37.4	185	3	US-08-950-720A-13
18	46	37.4	317	3	US-08-461-607-2
19	46	37.4	317	3	US-09-363-600-2
20	45	36.6	58	1	US-08-344-695-10
21	45	36.6	77	4	US-09-621-976-6430
22	45	36.6	280	4	US-09-352-991A-30950
23	45	36.6	589	1	US-07-668-648-2
24	45	36.6	589	2	US-08-429-998-2
25	45	36.6	589	2	US-08-431-333-2
26	45	36.6	589	5	PCT-US91-02321-2
27	45	36.6	593	1	US-07-668-648-4

28	45	36.6	593	2	US-08-429-998-4
29	45	36.6	593	2	US-08-431-333-4
30	45	36.6	593	4	US-08-991-862-17
31	45	36.6	593	5	PCT-US91-02321-4
32	45	36.6	2644	4	US-09-029-047C-2
33	44	36.2	316	3	US-08-801-344-4
34	44	36.2	316	4	US-09-498-599-4
35	44	36.2	316	4	US-08-477-383-54
36	44	35.8	16	1	US-08-487-174-54
37	44	35.8	16	1	US-08-480-750-54
38	44	35.8	16	3	US-09-219-446B-2
39	44	35.8	17	3	US-08-019-446B-3
40	44	35.8	19	1	US-08-084-848A-8
41	44	35.8	19	1	US-08-458-499-8
42	44	35.8	50	4	US-09-621-976-6430
43	44	35.8	63	3	US-08-488-799-93
44	44	35.8	63	3	US-09-488-799-97
45	44	35.8	63	3	US-09-488-799-99
46	44	35.8	68	1	US-08-137-800-48
47	44	35.8	68	1	US-08-477-383-48
48	44	35.8	68	1	US-08-487-174-48
49	44	35.8	68	1	US-08-480-750-48
50	44	35.8	68	1	US-08-480-750-48

## ALIGNMENTS

### RESULT 1

US-08-137-800-49  
; Sequence 49, Application US/08137800  
; Patent No. 5514774  
; GENERAL INFORMATION:  
; APPLICANT: Olivera, Baldomero M.  
; APPLICANT: Cruz, Lourdes J.  
; APPLICANT: Hillyard, David R.  
; APPLICANT: McIntosh, J. Michael  
; APPLICANT: Santos, Aneurina D.  
; TITLE OF INVENTION: Conotoxin Peptides  
; NUMBER OF SEQUENCES: 53  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti  
; STREET: 1201 New York Avenue N.W., Suite 1000  
; CITY: Washington  
; STATE: DC  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WordPerfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/137,800  
; FILING DATE: 19-OCT-1993  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ihnen, Jeffrey L.  
; REGISTRATION NUMBER: 28,957  
; REFERENCE/DOCKET NUMBER: 24260-104763  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-962-4810  
; TELEFAX: 202-962-8300  
; INFORMATION FOR SEQ ID NO: 49:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 70 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Conus sulcatus  
US-08-137-800-49

Sequence 4, Appli  
Sequence 4, Appli  
Sequence 17, Appl  
Sequence 17, Appl  
Sequence 2, Appli  
Sequence 4, Appli  
Sequence 4, Appli  
Sequence 54, Appl  
Sequence 54, Appl  
Sequence 54, Appl  
Sequence 2, Appli  
Sequence 3, Appli  
Sequence 8, Appli  
Sequence 8, Appli  
Sequence 6430, Ap  
Sequence 93, Appl  
Sequence 97, Appl  
Sequence 99, Appl  
Sequence 48, Appl  
Sequence 48, Appl  
Sequence 48, Appl

Query Match 40.7%; Score 50; DB 1; Length 70;  
 Best Local Similarity 46.7%; Pred. No. 7.5;  
 Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

5 CCLIPACRRNHKKFC 19  
 |||||:  
 52 CCSFPACRKYRPMC 66

ULT 2

US-08-487-383-49  
 Sequence 49, Application US/08477383  
 Patent No. 5589340  
 GENERAL INFORMATION:  
 APPLICANT: Olivera, Baldomero M.  
 APPLICANT: Cruz, Lourdes J.  
 APPLICANT: Hillyard, David R.  
 APPLICANT: Macintosh, J. Michael  
 APPLICANT: Santos, Ameurfino S.  
 TITLE OF INVENTION: Conotoxin Peptides  
 NUMBER OF SEQUENCES: 59  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Venable, Baetjer, Howard & Civiletti  
 STREET: 1201 New York Avenue, N.W., Suite 1000  
 CITY: Washington  
 STATE: DC  
 COUNTRY: U.S.A.  
 ZIP: 20005

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/477,383  
 FILING DATE: 07-JUN-1995  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/137,800  
 FILING DATE: 19-OCT-1993  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/084,848  
 FILING DATE: 29-JUN-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Ihnen, Jeffrey L.  
 REGISTRATION NUMBER: 28,957  
 REFERENCE/DOCKET NUMBER: 24260-107673  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-962-4810  
 TELEFAX: 202-962-8300  
 INFORMATION FOR SEQ ID NO: 49:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 70 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 HYPOTHETICAL: NO  
 ORIGINAL SOURCE:  
 ORGANISM: Conus sulcatus

US-08-477-383-49  
 Query Match 40.7%; Score 50; DB 1; Length 70;  
 Best Local Similarity 46.7%; Pred. No. 7.5;  
 Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

5 CCLIPACRRNHKKFC 19  
 |||||:  
 52 CCSFPACRKYRPMC 66

ULT 3

US-08-487-174-49  
 Sequence 49, Application US/08487174  
 Patent No. 5595972  
 GENERAL INFORMATION:  
 APPLICANT: Olivera, Baldomero M.  
 APPLICANT: Cruz, Lourdes J.  
 APPLICANT: Hillyard, David R.  
 APPLICANT: Macintosh, J. Michael  
 APPLICANT: Santos, Ameurfino S.  
 TITLE OF INVENTION: Conotoxin Peptides  
 NUMBER OF SEQUENCES: 59  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Venable, Baetjer, Howard & Civiletti  
 STREET: 1201 New York Avenue, N.W., Suite 1000  
 CITY: Washington  
 STATE: DC  
 COUNTRY: U.S.A.  
 ZIP: 20005  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/487,174  
 FILING DATE: 07-JUN-1995  
 CLASSIFICATION: 514  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/137,800  
 FILING DATE: 19-OCT-1993  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/084,848  
 FILING DATE: 29-JUN-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Ihnen, Jeffrey L.  
 REGISTRATION NUMBER: 28,957  
 REFERENCE/DOCKET NUMBER: 24260-107673  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-962-4810  
 TELEFAX: 202-962-8300  
 INFORMATION FOR SEQ ID NO: 49:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 70 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 HYPOTHETICAL: NO  
 ORIGINAL SOURCE:  
 ORGANISM: Conus sulcatus

US-08-487-174-49  
 Query Match 40.7%; Score 50; DB 1; Length 70;  
 Best Local Similarity 46.7%; Pred. No. 7.5;  
 Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Oy 5 CCLIPACRRNHKKFC 19  
 |||||:  
 Db 52 CCSFPACRKYRPMC 66

RESULT 4  
 US-08-480-750-49  
 Sequence 49, Application US/08480750  
 Patent No. 5633347  
 GENERAL INFORMATION:  
 APPLICANT: Olivera, Baldomero M.  
 APPLICANT: Cruz, Lourdes J.  
 APPLICANT: Hillyard, David R.  
 APPLICANT: Macintosh, J. Michael  
 APPLICANT: Santos, Ameurfino S.  
 TITLE OF INVENTION: Conotoxin Peptides  
 NUMBER OF SEQUENCES: 59

CORRESPONDENCE ADDRESS:  
ADDRESSES: Venable, Baetjer, Howard & Civiletti  
STREET: 1201 New York Avenue, N.W., Suite 1000  
CITY: Washington  
STATE: DC  
COUNTRY: U.S.A.  
ZIP: 20005

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/480,750  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 530

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/137,800  
FILING DATE: 19-OCT-1993

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/084,848  
FILING DATE: 29-JUN-1993

ATTORNEY/AGENT INFORMATION:  
NAME: Ihnen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: 24260-107673

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-962-4810  
TELEFAX: 202-962-8300

INFORMATION FOR SEQ ID NO: 49:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 70 amino acids  
TYPE: amino acid

STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO

ORIGINAL SOURCE:  
ORGANISM: Conus sulcatus  
38-480-750-49

Query Match 40.7%; Score 50; DB 1; Length 70;  
Best Local Similarity 46.7%; Pred. No. 7.5;  
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

5 CCLIPACRRNHKKFC 19  
||| ||| :  
52 CCSFPACRRYRPMC 66

ULT 5  
09-252-991A-26217  
Sequence 26217, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
EQ ID NO 26217  
LENGTH: 398  
TYPE: PRT  
ORGANISM: Pseudomonas aeruginosa  
09-252-991A-26217

Query Match 40.7%; Score 50; DB 4; Length 398;  
Best Local Similarity 46.7%; Pred. No. 7.5;  
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

5 CCLIPACRRNHKKFC 19  
||| ||| :  
52 CCSFPACRRYRPMC 66

ULT 5  
09-252-991A-26217  
Sequence 26217, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
EQ ID NO 26217  
LENGTH: 398  
TYPE: PRT  
ORGANISM: Pseudomonas aeruginosa  
09-252-991A-26217

Best Local Similarity 52.9%; Pred. No. 32;  
Matches 9; Conservative 1; Mismatches 3; Indels 4; Gaps 1;

QY 3 WRCCLPACRRNHKKFC 19  
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59 WRCC---CRRSPKGC 71

Db 59 WRCC---CRRSPKGC 71  
RESULT 6  
US-09-252-991A-20226  
Sequence 20226, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 20226  
LENGTH: 101  
TYPE: PRT  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-20226

Query Match 39.8%; Score 49; DB 4; Length 101;  
Best Local Similarity 72.7%; Pred. No. 14;  
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 WRCCLPACRR 13  
||| ||| :  
88 WRCCGTPACRR 98

Db 88 WRCCGTPACRR 98  
RESULT 7  
US-09-219-446B-9  
Sequence 9, Application US/09219446B  
Patent No. 6265541  
GENERAL INFORMATION:  
APPLICANT: Olivera, Baldomero M.  
APPLICANT: McIntosh, J. Michael  
APPLICANT: Yoshikami, Doju  
APPLICANT: Cartier, G. Edward  
APPLICANT: Luo, Siqin  
APPLICANT: University of Utah Research Foundation  
TITLE OF INVENTION: Uses of Alpha-Conotoxin Peptides  
FILE REFERENCE: Uses of Alpha-Conotoxins  
CURRENT APPLICATION NUMBER: US/09/219,446B  
CURRENT FILING DATE: 1998-12-23  
PRIOR APPLICATION NUMBER: US 60/080,598  
PRIOR FILING DATE: 1998-04-03  
PRIOR APPLICATION NUMBER: US 60/070,153  
PRIOR FILING DATE: 1997-12-31  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: Patent in Ver. 2.0  
SEQ ID NO 9  
LENGTH: 16  
TYPE: PRT  
ORGANISM: Conus purpurascens  
US-09-219-446B-9

Query Match 39.0%; Score 48; DB 3; Length 16;  
Best Local Similarity 40.0%; Pred. No. 3.9;  
Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 5 CCLIPACRRNHKKFC 19  
||| ||| :  
2 CCSLPCCANNPDYC 16

Db 2 CCSLPCCANNPDYC 16

JLT 8  
 09-252-991A-23844  
 sequence 23844, Application US/09252991A  
 atent No. 6551795  
 ENERAL INFORMATION:  
 APPLICANT: Marc J. Rubenfield et al.  
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
 FILE REFERENCE: 107196.136  
 CURRENT APPLICATION NUMBER: US/09/252,991A  
 CURRENT FILING DATE: 1999-02-18  
 PRIOR APPLICATION NUMBER: US 60/074,788  
 PRIOR FILING DATE: 1998-02-18  
 PRIOR APPLICATION NUMBER: US 60/094,190  
 PRIOR FILING DATE: 1998-07-27  
 NUMBER OF SEQ ID NOS: 33142  
 EQ ID NO 23844  
 LENGTH: 226  
 TYPE: PRT  
 ORGANISM: Pseudomonas aeruginosa  
 09-252-991A-23844  
 Query Match 39.0%; Score 48; DB 4; Length 226;  
 est Local Similarity 77.8%; Pred. No. 36;  
 atches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 2 NWRCLIPA 10  
 100 NWRCCASPA 108  
 ULT 9  
 09-270-391-16  
 sequence 16, Application US/09270391A  
 atent No. 6410233  
 ENERAL INFORMATION:  
 APPLICANT: de Belle, Ian  
 APPLICANT: Adamson, Eileen  
 APPLICANT: Mercola, Dan  
 TITLE OF INVENTION: Isolation and Identification of Control Sequences and  
 FILE REFERENCE: PS-00101.P.1  
 CURRENT APPLICATION NUMBER: US/09/270,391A  
 CURRENT FILING DATE: 1999-03-16  
 NUMBER OF SEQ ID NOS: 25  
 SOFTWARE: Patent In Ver. 2.0  
 EQ ID NO 16  
 LENGTH: 234  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 09-270-391-16  
 Query Match 39.0%; Score 48; DB 4; Length 234;  
 est Local Similarity 57.1%; Pred. No. 37;  
 atches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
 2 NWRCLIPACRNH 15  
 6 DYRCCLPPATHPH 19  
 SULT 10  
 -09-219-446B-10  
 Sequence 10, Application US/09219446B  
 Patent No. 6265541  
 GENERAL INFORMATION:  
 APPLICANT: Olivera, Baldomero M.  
 APPLICANT: McIntosh, J. Michael  
 APPLICANT: Yoshikami, Doju  
 APPLICANT: Cartier, G. Edward  
 APPLICANT: Luo, Siqin

APPLICANT: University of Utah Research Foundation  
 TITLE OF INVENTION: Uses of Alpha-Conotoxin Peptides  
 FILE REFERENCE: Uses of Alpha-Conotoxins  
 CURRENT APPLICATION NUMBER: US/09/219,446B  
 CURRENT FILING DATE: 1998-12-23  
 PRIOR APPLICATION NUMBER: US 60/080,588  
 PRIOR FILING DATE: 1998-04-03  
 PRIOR APPLICATION NUMBER: US 60/070,153  
 PRIOR FILING DATE: 1997-12-31  
 NUMBER OF SEQ ID NOS: 13  
 SOFTWARE: Patent In Ver. 2.0  
 EQ ID NO 10  
 LENGTH: 16  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Description of Artificial Sequence: A10L derivative  
 OTHER INFORMATION: of C. purpurascens PnIA  
 US-09-219-446B-10  
 Query Match 38.2%; Score 47; DB 3; Length 16;  
 Best Local Similarity 40.0%; Pred. No. 5.2;  
 Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;  
 QY 5 CCLIPACRNHHKFC 19  
 DB 2 CCSLPPCALNPDYC 16  
 RESULT 11  
 US-08-137-800-32  
 Sequence 32, Application US/08137800  
 Patent No. 5514774  
 GENERAL INFORMATION:  
 APPLICANT: Olivera, Baldomero M.  
 APPLICANT: Cruz, Lourdes J.  
 APPLICANT: Hilliard, David R.  
 APPLICANT: McIntosh, J. Michael  
 APPLICANT: Santos, Aneurquina D.  
 TITLE OF INVENTION: Conotoxin Peptides  
 NUMBER OF SEQUENCES: 53  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Venable, Baetjer, Howard & Civiletti  
 STREET: 1201 New York Avenue N.W., Suite 1000  
 CITY: Washington  
 STATE: DC  
 ZIP: 20005  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Wordperfect 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/137,800  
 FILING DATE: 19-OCT-1993  
 CLASSIFICATION: 530  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Ihnen, Jeffrey L.  
 REGISTRATION NUMBER: 28,957  
 REFERENCE/DOCKET NUMBER: 24260-104763  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-962-4810  
 TELEFAX: 202-962-8300  
 INFORMATION FOR SEQ ID NO: 32:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 18 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 ORIGINAL SOURCE:  
 ORGANISM: Conus ermineus



```

; OTHER INFORMATION: /note= "The C-terminus is
; OTHER INFORMATION: preferably amidated."
US-08--477-383-32
Query Match      37.4%; Score 46; DB 1; Length 18;
Best Local Similarity 46.7%; Pred. NO. 7.7;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY      5 CCLIPACRNNHKKFC 19
          ||||| : |
Db       4 CCSNPACNVNPFIC 18
          ||||| : |

RESULT 13
US-08-487-174-32
; Sequence 32, Application US/08487174
; Patent No. 5595972
; GENERAL INFORMATION:
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Cruz, Lourdes J.
; APPLICANT: Hillyard, David R.
; APPLICANT: Macintosh, J. Michael
; APPLICANT: Santos, Ameurfino S.
; TITLE OF INVENTION: Conotoxin Peptides
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti
; STREET: 1201 New York Avenue, N.W., Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,174
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/137,800
; FILING DATE: 19-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/084,848
; FILING DATE: 29-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24260-107673
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEetical: NO
; ORIGINAL SOURCE:
; ORGANISM: Conus ermineus
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 3
; OTHER INFORMATION: /note= "Xaa is Pro or Hydroxy-Pro."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 18
; OTHER INFORMATION: /note= "The C-terminus is
; OTHER INFORMATION: preferably amidated."

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JLT 17  
08-950-720A-13  
Sequence 13, Application US/08950720A  
Patent No. 6046028  
GENERAL INFORMATION:  
APPLICANT: Conklin, Darrell C.  
APPLICANT: Lofton-Day, Catherine E.  
APPLICANT: Lok, Si  
APPLICANT: Jaepers, Stephen R.  
TITLE OF INVENTION: INSULIN HOMOLOG  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ZymoGenetics, Inc.  
STREET: 1201 Eastlake Avenue East  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98102  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/950,720A  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Sawislak, Deborah A  
REGISTRATION NUMBER: 37,438  
REFERENCE/DOCKET NUMBER: 96-09  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-442-6672  
TELEFAX: 206-442-6678  
TELEX:  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 185 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: No. 6046028e  
08-950-720A-13  
Query Match 37.4%; Score 46; DB 3; Length 185;  
Best Local Similarity 43.8%; Pred. No. 55;  
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;  
4 RCCLIPACRNHHKFC 19  
:||||:|:|:  
170 KCCLIGCTKSLAKYC 185

ZIP: 33301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/461,607  
FILING DATE:  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/379,105  
FILING DATE:  
APPLICATION NUMBER: US 07/874,974  
FILING DATE: 27-APR-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Manso, Peter J.  
REGISTRATION NUMBER: 32,264  
REFERENCE/DOCKET NUMBER: IN21044-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 305-527-2498  
TELEFAX: 305-764-4996  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 317 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: Protein  
US-08-461-607-2  
Query Match 37.4%; Score 46; DB 3; Length 317;  
Best Local Similarity 66.7%; Pred. No. 87;  
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
QY 3 WECCLIPACRN 14  
DB 36 WRCTLIPIRRRD 47  
RESULT 19  
US-09-363-600-2  
Sequence 2, Application US/09363600  
Patent No. 6232524  
GENERAL INFORMATION:  
APPLICANT: Tischfield, Jay A.  
APPLICANT: Stambrook, Peter J.  
TITLE OF INVENTION: Live Animal Mutagenesis Systems for  
Testing Mutagenic Agents in Vivo  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &  
ADDRESSEE: Russell, P.A.  
STREET: 200 East Broward Boulevard  
CITY: Fort Lauderdale  
STATE: FL  
COUNTRY: USA  
ZIP: 33301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/363,600  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/461,607  
FILING DATE:  
APPLICATION NUMBER: US 07/874,974  
FILING DATE: 27-APR-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Manso, Peter J.

REGISTRATION NUMBER: 32,264  
REFERENCE/DOCKET NUMBER: IN21044-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 305-527-2498  
TELEFAX: 305-764-4996  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 317 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
39-363-600-2

Query Match 37.4%; Score 46; DB 3; Length 317;  
Best Local Similarity 66.7%; Pred. No. 87;  
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

3 WRCLIPACRN 14  
|||||  
36 WRCLIPRRRD 47

08-344-695-10  
sequence 10 Application US/08344695  
GENERAL INFORMATION:  
APPLICANT: O'BROCHTA, DAVID  
APPLICANT: WARREN, WILLIAM  
APPLICANT: ATKINSON, PETER  
TITLE OF INVENTION: A GENE TRANSFER SYSTEM FOR INSECTS  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,  
STREET: 1755 S. Jefferson Davis Highway, Suite 400  
CITY: Arlington  
STATE: Virginia  
COUNTRY: U.S.A.  
ZIP: 22202

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/344,695  
FILING DATE: 18-NOV-1994  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Kelber, Steven B.  
REGISTRATION NUMBER: 30,073  
REFERENCE/DOCKET NUMBER: 2747-058-27  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 413-3000  
TELEFAX: (703) 413-2220  
TELEX: 248855 OPAT UR  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 58 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
08-344-695-10

Query Match 36.6%; Score 45; DB 1; Length 58;  
Best Local Similarity 44.4%; Pred. No. 28;  
Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

2 NWRCCLIPACRNKKFC 19  
|||||  
2 NWAQCLLCPTRYSHKTC 19

RESULT 21  
US-09-621-976-4938  
; Sequence 4938, Application US/09621976  
; Patent No. 6639063  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Jobert, S.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
; FILE REFERENCE: GENSET.054PR2  
; CURRENT APPLICATION NUMBER: US/09/621,976  
; CURRENT FILING DATE: 2000-07-21  
; NUMBER OF SEQ ID NOS: 19335  
; SOFTWARE: Patent.pm  
; SEQ ID NO 4938  
; LENGTH: 77  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: UNSURE  
; LOCATION: 20  
; OTHER INFORMATION: Xaa = Met,Arg  
US-09-621-976-4938

Query Match 36.6%; Score 45; DB 4; Length 77;  
Best Local Similarity 50.0%; Pred. No. 35;  
Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 3 WRCCCLIPACRNHK 16  
|||||  
DB 8 WRCCCNFLCKREXK 21

RESULT 22  
US-09-252-991A-30950  
; Sequence 30950, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 30950  
; LENGTH: 280  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-30950

Query Match 36.6%; Score 45; DB 4; Length 280;  
Best Local Similarity 53.8%; Pred. No. 1.1e+02;  
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 4 RCCCLIPACRNHK 16  
|||||  
DB 61 RCCAGPACARSRR 73

RESULT 23  
US-07-668-648-2  
; Sequence 2, Application US/07668648  
; Patent No. 5416192  
; GENERAL INFORMATION:  
; APPLICANT: Shoyab, Mohammed  
; APPLICANT: Flowman, Gregory D.

```

/ NAME: Mirock, S. Leslie
/ REGISTRATION NUMBER: 18,872
/ REFERENCE/DOCKET NUMBER: 5624-161-999
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212)790-9090
/ TELEFAX: (212) 869-9741
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 589 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-429-998-2

Query Match 36.6%; Score 45; DB 2; Length 589;
Best Local Similarity 40.0%; Pred. No. 2e+02;
Matches 8; Conservative 3; Mismatches 7; Indels 2; Gaps 1;

QY 2 NWRCCLIP--ACRRNHKFC 19
:|||||:
Db 393 DWGCCPIPEAVCCLDHQCC 402
:|||||:

RESULT 25
US-08-431-333-2
: Sequence 2, Application US/08431333
: Patent No. 5965723
: GENERAL INFORMATION:
: APPLICANT: Shoyab, Mohammed
: APPLICANT: Plowman, Gregory D.
: TITLE OF INVENTION: EPITHELINS: NOVEL CYSTEINE-RICH GROWTH
: TITLE OF INVENTION: MODULATING PROTEINS
: NUMBER OF SEQUENCES: 12
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Pennie & Edmonds
: STREET: 1155 Avenue of the Americas
: CITY: New York
: STATE: New York
: COUNTRY: USA
: ZIP: 10036
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/431,333
: FILING DATE: 27-APR-1995
: CLASSIFICATION: 536
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/668,648
: FILING DATE: 13-MAR-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Mirock, S. Leslie
: REGISTRATION NUMBER: 18,872
: REFERENCE/DOCKET NUMBER: 5624-161-999
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212)790-9090
: TELEFAX: (212) 869-9741
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 589 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
/ US-08-431-333-2

Query Match 36.6%; Score 45; DB 2; Length 589;
Best Local Similarity 40.0%; Pred. No. 2e+02;
Matches 8; Conservative 3; Mismatches 7; Indels 2; Gaps 1;

QY 2 NWRCCLIP--ACRRNHKFC 19
:|||||:

```

383 DWGCCPIPEAVCCLDHQCC 402

ULT 26

US91-02321-2  
Sequence 2, Application PC/TUS9102321  
GENERAL INFORMATION:  
APPLICANT: Shoyab, Mohammed  
TITLE OF INVENTION: EPIITHELINS: NOVEL CYSTEINE-RICH GROWTH  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Bristol-Myers Squibb Company  
STREET: 3005 First Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98121

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US91/02321  
FILING DATE: 19910403  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Poor, Brian W.  
REGISTRATION NUMBER: 32,928  
REFERENCE/DOCKET NUMBER: ON0071A-PC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 728-4800  
TELEFAX: (206) 448-4775

INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 589 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: protein

US91-02321-2

Query Match 36.6%; Score 45; DB 5; Length 589;

Best Local Similarity 40.0%; Pred. No. 2e+02;

Matches 8; Conservative 3; Mismatches 7; Indels 2; Gaps 1;

2 NWRCCLIP--ACRRNHKKFC 19

383 DWGCCPIPEAVCCLDHQCC 402

ULT 27

07-668-648-4  
Sequence 4, Application US/07668648  
Patent No. 5416192  
GENERAL INFORMATION:  
APPLICANT: Shoyab, Mohammed  
TITLE OF INVENTION: EPIITHELINS: NOVEL CYSTEINE-RICH GROWTH  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/668,648  
FILING DATE: 19910819  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Mistrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 5624-161-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741

INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 593 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: protein

US-07-668-648-4

Query Match 36.6%; Score 45; DB 1; Length 593;

Best Local Similarity 42.1%; Pred. No. 2e+02;

Matches 8; Conservative 2; Mismatches 7; Indels 2; Gaps 1;

3 WRCCLIP--ACRRNHKKFC 19

386 WGCCPIPEAVCCLDHQCC 404

RESULT 28

US-08-429-998-4

Sequence 4, Application US/08429998

Patent No. 5885961

GENERAL INFORMATION:

APPLICANT: Shoyab, Mohammed

APPLICANT: Plowman, Gregory D.

TITLE OF INVENTION: EPIITHELINS: NOVEL CYSTEINE-RICH GROWTH

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 728-4800

TELEFAX: (206) 448-4775

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 589 amino acids

TYPE: AMINO ACID

TOPOLOGY: linear

MOLECULE TYPE: protein

US91-02321-2

Query Match 36.6%; Score 45; DB 5; Length 589;

Best Local Similarity 40.0%; Pred. No. 2e+02;

Matches 8; Conservative 3; Mismatches 7; Indels 2; Gaps 1;

2 NWRCCLIP--ACRRNHKKFC 19

383 DWGCCPIPEAVCCLDHQCC 402

ULT 27

07-668-648-4

Sequence 4, Application US/07668648

Patent No. 5416192

GENERAL INFORMATION:

APPLICANT: Shoyab, Mohammed

APPLICANT: Plowman, Gregory D.

TITLE OF INVENTION: EPIITHELINS: NOVEL CYSTEINE-RICH GROWTH

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 593 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-429-998-4

[illegible]

CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Poor, Brian W.  
REGISTRATION NUMBER: 32,928  
REFERENCE/DOCKET NUMBER: 080071A-PC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)728-4800  
TELEFAX: (206)448-4775  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 593 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
-US91-02321-4

Query Match 36.6%; Score 45; DB 5; Length 593;  
Best Local Similarity 42.1%; Pred. No. 2e+02;  
Matches 8; Conservative 2; Mismatches 7; Indels 7; Gaps 1;

3 WRCLIP--ACRRNHHKFC 19  
386 WGCOPIEAVCCSDHQHCC 404

ULT 33  
09-029-047C-2  
Sequence 2, Application US/09029047C  
Patent No. 6832336  
GENERAL INFORMATION:  
APPLICANT: Cart, Antony M.  
TITLE OF INVENTION: Cell-Cycle Checkpoint Genes  
FILE REFERENCE: 27866/34132  
CURRENT APPLICATION NUMBER: US/09/029,047C  
CURRENT FILING DATE: 1999-05-11  
PRIOR APPLICATION NUMBER: PCT/GB96/02197  
PRIOR FILING DATE: 1996-09-06  
PRIOR APPLICATION NUMBER: GB 9518220.0  
PRIOR FILING DATE: 1995-09-06  
NUMBER OF SEQ ID NOS: 14  
SOFTWARE: PatentIn Ver. 3.1  
SEQ ID NO 2  
LENGTH: 2644  
TYPE: PRT  
ORGANISM: Homo sapiens  
09-029-047C-2

Query Match 36.6%; Score 45; DB 4; Length 2644;  
Best Local Similarity 37.5%; Pred. No. 7e+02;  
Matches 9; Conservative 1; Mismatches 8; Indels 6; Gaps 1;

2 NW-----RCCLIPACRRNHHKFC 19  
101 NWIITRLRIIAATPSCHLLHKIC 124

SULT 34  
08-801-344-4  
Sequence 4, Application US/08801344  
Patent No. 6087140  
GENERAL INFORMATION:  
APPLICANT: Cameron, Douglas C.  
APPLICANT: Shaw, Anita J.  
APPLICANT: Altaras, Nedim E.  
TITLE OF INVENTION: MICROBIAL PRODUCTION OF 1,2-PROPANEDIOL  
FROM SUGAR  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Dewitt Ross & Stevens S.C.  
STREET: 8000 Excelsior Drive, Suite 401  
CITY: Madison  
STATE: WI  
COUNTRY: U.S.A.

ZIP: 53717-1914  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/801,344  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Sara, Charles S.  
REFERENCE/DOCKET NUMBER: 09820.037  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 608-831-2100  
TELEFAX: 608-831-2106  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 316 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Rat lens aldose reductase  
US-08-801-344-4

Query Match 36.2%; Score 44.5; DB 3; Length 316;  
Best Local Similarity 41.2%; Pred. No. 1.4e+02;  
Matches 7; Conservative 4; Mismatches 5; Indels 1; Gaps 1;

QY 2 NWRCLIPACRRNHHKFC 18  
DB 295 NWEVCALMSCAK-HKDY 310

RESULT 35  
US-09-498-599-4  
Sequence 4, Application US/09498599  
Patent No. 6303352  
GENERAL INFORMATION:  
APPLICANT: Cameron, Douglas C.  
APPLICANT: Shaw, Anita J.  
APPLICANT: Altaras, Nedim E.  
TITLE OF INVENTION: MICROBIAL PRODUCTION OF  
1,2-PROPANEDIOL FROM SUGAR  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dewitt Ross & Stevens S.C.  
STREET: 8000 Excelsior Drive, Suite 401  
CITY: Madison  
STATE: WI  
COUNTRY: U.S.A.  
ZIP: 53717-1914  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/498,599  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Sara, Charles S.  
REFERENCE/DOCKET NUMBER: 09820.037  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 608-831-2100  
TELEFAX: 608-831-2106  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:



LENGTH: 316 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Rat lens aldose reductase  
J9-498-599-4

very Match 36.2%; Score 44.5; DB 4; Length 316;  
ast Local Similarity 41.2%; Pred. No. 1.4e+02;  
atches 7; Conservative 4; Mismatches 5; Indels 1; Gaps 1;

2 NWRCCCLIPACRRNHKXF 18  
||| : : : :  
295 NWRVCAALMSCAK-HCY 310

rch completed: February 18, 2004, 06:08:05  
time : 43 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

protein - protein search, using sw model

on: February 18, 2004, 06:16:09 ; Search time 21 Seconds  
(without alignments)  
87.030 Million cell updates/sec

le: US-09-806-376-1

fect score: 123

uence: 1 FNRCCCLIPACRRNHKKFC 19

ring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

arched: 283366 seqs, 96191526 residues

al number of hits satisfying chosen parameters: 3435

imum DB seq length: 0

imum DB seq length: 19

st-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

atabase :

PIR 78:\*

1: Pirl:\*

2: Pirl:\*

3: Pirl:\*

4: Pirl:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

alt	No.	Score	Query	Match	Length	DB	ID	Description
1	48	39.0	16	2	A54877			alpha-conotoxin Pn
2	44	35.8	16	2	A59046			alpha-conotoxin MI
3	44	35.8	16	2	A59042			alpha-conotoxin Ep
4	42	34.1	16	2	B54877			alpha-conotoxin Pn
5	40	32.5	18	1	A58589			alpha-conotoxin EI
6	38	30.9	16	2	A59045			alpha-conotoxin Au
7	38	30.9	19	2	A4379			alpha-conotoxin SI
8	37.5	30.5	14	1	NTKNLM			alpha-conotoxin MI
9	37	30.1	16	2	C59045			alpha-conotoxin Au
10	31	25.2	13	1	NTKNAS			alpha-conotoxin SI
11	31	25.2	15	1	NTKNAG			alpha-conotoxin GI
12	30	24.4	15	2	B59045			alpha-conotoxin Au
13	29.5	24.0	14	2	A58963			alpha-conotoxin Cn
14	28	22.8	12	1	A53709			alpha-conotoxin Im
15	27.5	22.4	17	2	A54534			heat-stable entero
16	27	22.0	16	2	PH1781			T cell receptor al
17	27	22.0	18	1	QHEC2			heat-stable entero
18	26	21.1	9	2	A29477			diuretic neuropt
19	26	21.1	12	2	A33900			hydrin 1 - African
20	26	21.1	13	1	NTKN2G			alpha-conotoxin GI
21	26	21.1	19	2	C21182			4K prothoracitro
22	25.5	20.7	18	2	A60103			heat-stable entero
23	25	20.3	13	2	A28953			alpha-conotoxin SI
24	24	19.5	8	2	A54823			olfactory receptor
25	24	19.5	8	2	B54823			olfactory receptor
26	24	19.5	11	2	S61797			T-cell-specific tr
27	24	19.5	19	2	A58700			actagardine [valid
28	23	18.7	9	2	B28495			conopressin S - co
29	23	18.7	11	2	T06383			hypothetical prote

ALIGNMENTS

RESULT 1

A54877 alpha-conotoxin PnIA [validated] - cone shell (Conus pennaceus)

N/Alternate names: alpha-Crx-PnIA

C/Species: Conus pennaceus

C/Date: 19-Mar-1997 #sequence\_revision 25-Apr-1997 #text\_change 15-Sep-2000

C/Accession: A54877

R/Painzilber, M.; Hasson, A.; Oren, R.; Burlingame, A.L.; Gordon, D.; Spira, M.E.; Zlot

Biochemistry 33, 9523-9529, 1994

A/Title: New mollusc-specific alpha-conotoxins block Aplysia neuronal acetylcholine rec

A/Reference number: A54877; MUID:94347719; PMID:8068627

A/Accession: A54877

A/Molecule type: protein

A/Residues: 1-16 <FAI>

R/Hu, S.H.; Gehrmann, J.; Guddat, L.W.; Alewood, P.F.; Craik, D.J.; Martin, J.L.

submitted to the Brookhaven Protein Data Bank, January 1996

A/Reference number: A66355; PDB:1PEN

A/Comment: This alpha-conotoxin, as an acetylcholine receptor inhibitor, is a postsynap

C/Superfamily: alpha-conotoxin

C/Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neurc

F:2-8,3-16/Disulfide bonds: #status experimental

F:16/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 39.0%; Score 48; DB 2; Length 16;

Best Local Similarity 40.0%; Pred. NO. 1.6;

Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 5 CCLIPACRRNHKKFC 19

Db 2 CCSLPPCAANNPDYC 16

RESULT 2

A59046

alpha-conotoxin MII - cone shell (Conus magus)

C/Species: Conus magus (magus cone)

C/Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 16-Jul-1999

C/Accession: A59046

R/Carter, G.E.; Yoshikami, D.; Gray, W.R.; Luo, S.; Olivera, B.M.; McIntosh, J.M.

J. Biol. Chem. 271, 7522-7528, 1996

A/Title: A new alpha-conotoxin which targets alpha3beta2 nicotinic acetylcholine recept

A/Reference number: A59046; MUID:96205934; PMID:8631783

A/Accession: A59046

A/Status: Preliminary

A/Molecule type: protein

A/Residues: 1-16 <CAR>

RESULT 5  
 AS8589  
 alpha-conotoxin EI - cone shell (Conus ermineus)  
 C/Species: Conus ermineus (ermine cone)  
 C/Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
 C/Accession: A58589  
 R/Martinez, J.S.; Olivera, B.M.; Gray, W.R.; Craig, A.G.; Groebe, D.R.; Abramson, S.N.;  
 Biochemistry 34, 14519-14526, 1995  
 A/Title: alpha-Conotoxin EI, a new nicotinic acetylcholine receptor antagonist with novel  
 A/Reference number: A58589; MUID:96062516; PMID:7578057  
 A/Accession: A58589  
 A/Molecule type: protein  
 A/Residues: 1-18 <VAR>  
 A/Note: sequence confirmed by chemical synthesis  
 C/Comment: This alpha-conotoxin, as an acetylcholine receptor inhibitor, is a postsynaptic  
 C/Superfamily: alpha-conotoxin  
 C/Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; hydroxyproline; pc  
 F/3/Modified site: 4-hydroxyproline (Pro) #status experimental  
 F/4-10-15/Disulfide bonds: #status experimental  
 F/18/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 32.5%; Score 40; DB 1; Length 18;  
 Best Local Similarity 33.3%; Pred. No. 25;  
 Matches 5; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 5 CCLIPACRRNHKKFC 19  
 ||| |::|  
 Db 4 CCYHPTCNMSNPQIC 18  
 ||| |::|

RESULT 6  
 A59045  
 alpha-conotoxin AUIA - cone shell (Conus aulicus)  
 C/Species: Conus aulicus (Court cone)  
 C/Date: 23-Jul-1999 #sequence\_revision 23-Jul-1999 #text\_change 23-Jul-1999  
 C/Accession: A59045  
 R/Luo, S.; Kulak, J.M.; Carrier, G.E.; Jacobsen, R.B.; Yoshikami, D.; Olivera, B.M.; Mc  
 J. Neurosci. 18, 8571-8579, 1998  
 A/Title: Alpha-conotoxin AUIB selectively blocks alpha3beta4 nicotinic acetylcholine re  
 A/Reference number: A59045; MUID:99003392; PMID:9786965  
 A/Accession: A59045  
 A/Status: preliminary  
 A/Molecule type: protein  
 A/Residues: 1-16 <LUO>  
 C/Superfamily: alpha-conotoxin  
 C/Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neuro  
 F/1-16/Product: alpha-conotoxin AUIA #status experimental <MAT>  
 F/2-8-15/Disulfide bonds: #status experimental  
 F/16/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 30.9%; Score 38; DB 2; Length 16;  
 Best Local Similarity 33.3%; Pred. No. 44;  
 Matches 5; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 5 CCLIPACRRNHKKFC 19  
 ||| |::|  
 Db 2 CCSYPPCFATNSDYC 16  
 ||| |::|

RESULT 7  
 A44379  
 alpha-conotoxin SII - cone shell (Conus striatus)  
 C/Species: Conus striatus (striated cone)  
 C/Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 16-Jul-1999  
 C/Accession: A44379  
 R/Ramilo, C.A.; Zafaralla, G.C.; Nadaesi, L.; Hammerland, L.G.; Yoshikami, D.; Gray, W  
 Biochemistry 31, 9919-9926, 1992  
 A/Title: Novel alpha- and omega-conotoxins from Conus striatus venom.  
 A/Reference number: A44379; MUID:93003172; PMID:1390774  
 A/Accession: A44379  
 A/Molecule type: protein  
 A/Residues: 1-19 <RAM>  
 A/Cross-references: CAS:143294-31-9; PIDN:AAB23762-1; PID:g257934

Experimental source: venom  
 Note: sequence extracted from NCBI backbone (NCBIP:116000); structure confirmed by chemo  
 Comment: This peptide is an acetylcholine receptor blocker.  
 Superfamily: alpha-conotoxin  
 Keywords: acetylcholine receptor inhibitor; postsynaptic neurotoxin; venom  
 -18,3-8,4-14/Disulfide bonds: #status predicted  
 9/Modified site: amidated carboxyl end (Ser) #status absent

Query Match 30.9%; Score 38; DB 2; Length 19;  
 Best Local Similarity 54.5%; Pred. No. 50;  
 Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

5 CCLIPACRRNH 15  
 |||||  
 2 CCNCPACGPNY 12

ULT 8  
 NIM

Alpha-conotoxin MI - cone shell (Conus magus)  
 Species: Conus magus (magus cone)  
 Date: 18-Apr-1984 #sequence\_revision 18-Apr-1984 #text\_change 16-Jul-1999  
 Accession: A01784  
 McIntosh, M.; Cruz, L.J.; Hunkapiller, M.W.; Gray, W.R.; Olivera, B.M.  
 J. Biochem. Biophys. 218, 329-334, 1992  
 Title: Isolation and structure of a peptide toxin from the marine snail Conus magus.  
 Reference number: A90071; MUID:83073456; PMID:7149738  
 Accession: A01784  
 Molecule type: protein  
 Residues: 1-14 <NCI>  
 Gray, W.R.; Rivier, J.E.; Galyean, R.; Cruz, L.J.; Olivera, B.M.  
 Biol. Chem. 258, 12247-12251, 1983  
 Title: Conotoxin MI. Disulfide bonding and conformational states.  
 Reference number: A92396; MUID:84032400; PMID:6630187  
 Contents: annotation; disulfide bonds  
 Comment: This alpha-conotoxin, as an acetylcholine receptor inhibitor, is a postsynaptic  
 Superfamily: alpha-conotoxin  
 Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neuroto  
 -8,4-14/Disulfide bonds: #status experimental  
 4/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 30.5%; Score 37.5; DB 1; Length 14;  
 Best Local Similarity 58.3%; Pred. No. 47;  
 Matches 7; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

4 RCCLIPACRRNH 15  
 |||||  
 2 RCC-HPACGKNY 12

ULT 9  
 3045

Alpha-conotoxin AuIC - cone shell (Conus aulicus)  
 Species: Conus aulicus (court cone)  
 Date: 23-Jul-1999 #sequence\_revision 23-Jul-1999 #text\_change 23-Jul-1999  
 Accession: C59045  
 Juo, S.; Kulak, J.M.; Cartier, G.E.; Jacobsen, R.B.; Yoshikami, D.; Olivera, B.M.; McInt  
 Neurosci. 18, 8571-8579, 1998  
 Title: Alpha-conotoxin AuIB selectively blocks alpha3beta4 nicotinic acetylcholine rec  
 Reference number: A59045; MUID:99003392; PMID:9788965  
 Accession: C59045  
 Status: preliminary  
 Molecule type: protein  
 Residues: 1-16 <LUO>  
 Superfamily: alpha-conotoxin  
 Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neuro  
 1-16/Product: alpha-conotoxin AuIC #status experimental <MAT>  
 2-8,3-16/Disulfide bonds: #status experimental  
 16/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 30.1%; Score 37; DB 2; Length 16;  
 Best Local Similarity 33.3%; Pred. No. 61;  
 Matches 5; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 5 CCLIPACRRNHKKFC 19  
 |||||  
 Db 2 CCSVPPCFATNSOYC 16

RESULT 10  
 NTKNAS  
 Alpha-conotoxin SIA - cone shell (Conus striatus)  
 Species: Conus striatus (striated cone)  
 C>Date: 30-Sep-1992 #sequence\_revision 30-Sep-1992 #text\_change 23-May-1997  
 C/Accession: A40312  
 R/Myers, R.A.; Zafaralla, G.C.; Gray, W.R.; Abbott, J.; Cruz, L.J.; Olivera, B.M.  
 Biochemistry 30, 9370-9377, 1991  
 A>Title: alpha-Conotoxins, small peptide probes of nicotinic acetylcholine receptors.  
 F:2-7,3-13/Disulfide bonds: #status experimental  
 A/Reference number: A40312; MUID:91369955; PMID:1892838  
 A/Accession: A40312  
 A/Molecule type: protein  
 A/Residues: 1-13 <MYE>  
 C/Comment: This paralytic toxin from a fish-hunting cone snail inhibits the acetylcholi  
 C/Superfamily: alpha-conotoxin  
 C/Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neuro  
 F:2-7,3-13/Disulfide bonds: #status experimental  
 F:13/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 25.2%; Score 31; DB 1; Length 13;  
 Best Local Similarity 55.6%; Pred. No. 3.8e+02;  
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 CLIPACRRN 14  
 |||||  
 Db 2 CCHPACGKN 10

RESULT 11  
 NTKNAG  
 Alpha-conotoxin GIA [validated] - cone shell (Conus geographus)  
 N/Alternate names: alpha-Crx-GIA  
 N/Contents: alpha-conotoxin GI  
 C/Species: Conus geographus (geography cone)  
 C/Date: 24-Sep-1981 #sequence\_revision 24-Sep-1981 #text\_change 15-Sep-2000  
 C/Accession: A01782  
 R/Gray, W.R.; Luque, A.; Olivera, B.M.; Barrett, J.; Cruz, L.J.  
 J. Biol. Chem. 256, 4734-4740, 1981  
 A>Title: Peptide toxins from Conus geographus venom.  
 A/Reference number: A92320; MUID:81191854; PMID:7014556  
 A/Accession: A01782  
 A/Molecule type: protein  
 A/Residues: 1-15 <GRA>  
 R/Gray, W.R.; Rivier, J.E.; Galyean, R.; Cruz, L.J.; Olivera, B.M.  
 J. Biol. Chem. 258, 12247-12251, 1983  
 A>Title: Conotoxin MI. Disulfide bonding and conformational states.  
 A/Reference number: A92396; MUID:84032400; PMID:6630187  
 A/Contents: annotation; disulfide bonds  
 R/Guddat, L.W.; Shan, L.; Martin, J.L.; Edmundson, A.B.; Gray, W.R.  
 submitted to the Brookhaven Protein Data Bank, May 1996  
 A/Reference number: A68253; PDB:1NOT  
 A/Contents: annotation; X-ray crystallography, 1.2 angstroms, residues 1-13  
 R/Guddat, L.W.; Martin, J.A.; Shan, L.; Edmundson, A.B.; Gray, W.R.  
 Biochemistry 35, 11329-11335, 1996  
 A>Title: Three-dimensional structure of the alpha-conotoxin GI at 1.2 angstroms resolut  
 A/Reference number: A58592; MUID:96378624; PMID:8784187  
 A/Contents: annotation; X-ray crystallography, 1.2 angstroms  
 R/Pardi, A.; Galdes, A.; Florance, J.; Manicotte, D.  
 Biochemistry 28, 5494-5501, 1989  
 A>Title: Solution structures of alpha-conotoxin GI determined by two-dimensional NMR sp  
 A/Reference number: A30629; MUID:89375269; PMID:2775719  
 A/Contents: annotation; conformation by (1)H-NMR  
 C/Comment: This alpha-conotoxin, as an acetylcholine receptor inhibitor, is a postsynap  
 C/Superfamily: alpha-conotoxin  
 C/Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; blocked carboxyl e  
 F:1-15/Product: conotoxin GIA #status experimental <GRA>  
 F:1-13/Product: conotoxin GI #status experimental <GIC>

2-7,3-13/Disulfide bonds: #link GIA #status predicted  
 2-7,3-13/Disulfide bonds: #link GIC #status experimental  
 13/Modified site: amidated carboxyl end (Cys) (amide in mature form from following cly  
 15/Modified site: blocked carboxyl end (Lys) (probably amidated) #status experimental

Query Match 25.2%; Score 31; DB 1; Length 15;  
 Best Local Similarity 50.0%; Pred. No. 4.2e+02;  
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

6 CLIPACRRH 15  
 2 CCNPACRRH 11

## SULT 12

9045  
 Pha-conotoxin AuIB - cone shell (Conus aulicus)  
 Species: Conus aulicus (Court cone)  
 Date: 23-Jul-1999 #sequence\_revision 23-Jul-1999 #text\_change 23-Jul-1999  
 Luo, S.; Kulak, J.M.; Cartier, G.E.; Jacobsen, R.B.; Yoshikami, D.; Olivera, B.M.; McI  
 Neurosci. 18, 8571-8579, 1998  
 Title: Alpha-conotoxin AuIB selectively blocks alpha3beta4 nicotinic acetylcholine rec  
 Reference number: A59045; MUID:99003392; PMID:9786965  
 Accession: B59045  
 Status: preliminary  
 Molecule type: protein  
 Residues: 1-15 <LUO>  
 Superfamily: alpha-conotoxin  
 Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neuro  
 1-15/Product: alpha-conotoxin AuIB #status experimental <MAT>  
 2-8,3-15/Disulfide bonds: #status experimental  
 15/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 24.4%; Score 30; DB 2; Length 15;  
 Best Local Similarity 57.1%; Pred. No. 5.8e+02;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

5 CCLIPAC 11  
 2 CCYPPC 8

## SULT 13

8963  
 Pha-conotoxin CnIA - cone shell (Conus consors)  
 Contains: alpha-conotoxin CnIB  
 Species: Conus consors  
 Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 16-Jul-1999  
 Favreau, P.; Krimm, I.; Le Gall, F.; Bobenrieth, M.J.; Lamhanh, H.; Bouet, F.; Servet  
 ochimistry 38, 6317-6326, 1999  
 Title: Biochemical characterization and nuclear magnetic resonance structure of novel  
 Reference number: A58963; MUID:99255390; PMID:10320362  
 Accession: A58963  
 Status: preliminary  
 Molecule type: protein  
 Residues: 1-14 <FAV>  
 Superfamily: alpha-conotoxin  
 Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neuro  
 1-14/Product: alpha-conotoxin CnIA #status experimental <MAT>  
 3-14/Product: alpha-conotoxin CnIB #status experimental <MAT>  
 3-8,4-14/Disulfide bonds: #status experimental  
 14/Modified site: amidated carboxyl end (Cys) #status experimental

4 RCCLIPAC 11  
 2 RCC-HPAC 8

Query Match 24.0%; Score 29.5; DB 2; Length 14;  
 Best Local Similarity 75.0%; Pred. No. 6.5e+02;  
 Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

## RESULT 14

A53709  
 Alpha-conotoxin ImI - cone shell (Conus imperialis)  
 N Alternate names: alpha-Cnx-ImI  
 C Species: Conus imperialis (Imperial cone)  
 C Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
 R; McIntosh, J.M.; Yoshikami, D.; Mahe, E.; Nielsen, D.B.; Rivier, J.E.; Gray, W.R.; Oli  
 J. Biol. Chem. 269, 16733-16739, 1994  
 A Title: A nicotinic acetylcholine receptor ligand of unique specificity, alpha-conotox  
 A Reference number: A53709; MUID:94266899; PMID:8206995  
 A Accession: A53709  
 A Molecule type: protein  
 A Residues: 1-12 <MC>  
 A Note: structure confirmed by chemical synthesis  
 C Comment: This alpha-conotoxin, as an acetylcholine receptor inhibitor, is a postsynap  
 C Superfamily: alpha-conotoxin  
 C Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neuro  
 F 2-8,3-12/Disulfide bonds: #status experimental  
 F 12/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 22.8%; Score 28; DB 1; Length 12;  
 Best Local Similarity 57.1%; Pred. No. 9.6e+02;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 CCLIPAC 11  
 DB 2 CCSPPC 8

## RESULT 15

A54534  
 heat-stable enterotoxin - Vibrio mimicus (fragment)  
 C Species: Vibrio mimicus  
 C Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 03-May-1996  
 C Accession: A54534  
 R; Arita, M.; Honda, T.; Miwatani, T.; Takeda, T.; Takao, T.; Shimonishi, Y.  
 FEMS Microbiol. Lett. 79, 105-110, 1991  
 A Title: Purification and characterization of a heat-stable enterotoxin of Vibrio mimic  
 A Reference number: A54534  
 A Accession: A54534  
 A Status: preliminary  
 A Molecule type: protein  
 A Residues: 1-17 <ARI>  
 C Superfamily: heat-stable enterotoxin ST

Query Match 22.4%; Score 27.5; DB 2; Length 17;  
 Best Local Similarity 60.0%; Pred. No. 1.5e+03;  
 Matches 6; Conservative 0; Mismatches 1; Indels 3; Gaps 1;

QY 5 CCLIPAC 11  
 DB 3 CCEICCNFAC 12

## RESULT 16

PH1781  
 T cell receptor alpha chain V region (clone 2DN V alpha 24-2) - human (fragment)  
 C Species: Homo sapiens (man)  
 C Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 16-Jul-1999  
 C Accession: PH1781  
 R; Porcelli, S.; Yockey, C.E.; Brenner, M.B.; Balk, S.P.  
 J. Exp. Med. 178, 1-16, 1993  
 A Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blood

Query Match 22.0%; Score 27; DB 2; Length 16;  
 Best Local Similarity 75.0%; Pred. No. 6.5e+02;  
 Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

4 RCCLIPAC 11  
 2 RCC-HPAC 8

est Local Similarity 38.5%; Pred. No. 1.6e+03;  
 arches 5; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

6 CLIPACRRNHKKF 18  
 ::|||::|  
 3 CVVRAPRDNDKRF 15

ULT 17  
 C2  
 t-stable enterotoxin ST-2 - Escherichia coli  
 Species: Escherichia coli  
 Date: 06-Jul-1982 #sequence\_revision 06-Jul-1982 #text\_change 31-Dec-1996  
 Accession: A01823  
 Han, S.K.; Giannella, R.A.  
 Biol. Chem. 256, 7744-7746, 1981  
 Title: Amino acid sequence of heat-stable enterotoxin produced by Escherichia coli pat  
 reference number: A01823; PMID:81264141; PMID:7021541  
 Accession: A01823  
 Molecule type: protein  
 Residues: 1-18 <CHA>  
 Experimental source: strain 18D, serotype 0.42:k86:H37  
 Comment: This enterotoxin is one of several, of differing molecular sizes, produced by  
 es of the heat-stable enterotoxin ST-1.  
 Superfamily: heat-stable enterotoxin ST  
 Keywords: enterotoxin; heat-stable protein  
 -18/Product: heat-stable enterotoxin ST-2 #status experimental <MAT>  
 -10,6-14,9-17/Disulfide bonds: #status predicted

Query Match 22.0%; Score 27; DB 1; Length 18;  
 Best Local Similarity 66.7%; Pred. No. 1.8e+03;  
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

6 CLIPAC 11  
 |||||  
 9 CCYPAC 14

SULT 18  
 2477  
 ionic neuropeptide F1 - migratory locust  
 Species: Locusta migratoria (migratory locust)  
 Date: 31-Dec-1988 #sequence\_revision 31-Dec-1988 #text\_change 31-Dec-1993  
 Accession: A29477  
 Proulx, J.P.; Miller, C.A.; Li, J.P.; Carney, R.L.; Girardie, A.; Delaage, M.; Schooley  
 Chem. Biophys. Res. Commun. 149, 180-186, 1987  
 Title: Identification of an arginine vasopressin-like diuretic hormone from Locusta mi  
 Reference number: A29477; PMID:88077077; PMID:3689410  
 Accession: A29477  
 Molecule type: protein  
 Residues: 1-9 <PRO>  
 Note: two neuropeptides, F1 and F2, were identified. F2 is an antiparallel dimer of F1  
 Keywords: neuropeptide

Query Match 21.1%; Score 26; DB 2; Length 9;  
 Best Local Similarity 62.5%; Pred. No. 2.8e+05;  
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

6 CLIPACRR 13  
 |||||  
 1 CLITNCPR 8

SULT 19  
 3900  
 drin 1 - African clawed frog  
 Alternate names: arginine-vasotocin-related peptide; vasotocinyl-Gly-Lys  
 Species: Xenopus laevis (African clawed frog)  
 Date: 09-Mar-1990 #sequence\_revision 09-Mar-1990 #text\_change 31-Mar-1997  
 Accession: A33900; S30176  
 Rouille, Y.; Michel, G.; Chauvet, M.T.; Chauvet, J.; Acher, R.  
 oc. Natl. Acad. Sci. U.S.A. 86, 5272-5275, 1989  
 Title: Hydrins, hydroosmotic neurohypophysial peptides: osmoregulatory adaptation in a

A;Reference number: A33900; PMID:89315779; PMID:2787509  
 A;Accession: A33900  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-12 <ROU>  
 R;Iwamuro, S.; Hayashi, H.; Kikuyama, S.  
 Biochim. Biophys. Acta 1176, 143-147, 1993  
 A;Title: An additional arginine-vasotocin-related peptide, vasotocinyl-Gly-Lys, in Xenc  
 A;Reference number: S30176; PMID:93200145; PMID:8452872  
 A;Accession: S30176  
 A;Molecule type: protein  
 A;Residues: 1-12 <IWA>  
 C;Keywords: neuropeptide

Query Match 21.1%; Score 26; DB 2; Length 12;  
 Best Local Similarity 41.7%; Pred. No. 1.8e+03;  
 Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 6 CLIPACRRNHKK 17  
 |||||  
 Db 1 CYTONCPRGGR 12

RESULT 20  
 NTKN2G  
 alpha-conotoxin GII - cone shell (Conus geographus)  
 C;Species: Conus geographus (geography cone)  
 C;Date: 24-Sep-1981 #sequence\_revision 24-Sep-1981 #text\_change 23-May-1997  
 C;Accession: A01783  
 R;Gray, W.R.; Luque, A.; Olivera, B.M.; Barrett, J.; Cruz, L.J.  
 J. Biol. Chem. 256, 4734-4740, 1981  
 A;Title: Peptide toxins from Conus geographus venom.  
 A;Reference number: A92320; PMID:81191854; PMID:7014556  
 A;Accession: A01783  
 A;Molecule type: protein  
 A;Residues: 1-13 <GRA>  
 R;Gray, W.R.; Rivier, J.E.; Galyean, R.; Cruz, L.J.; Olivera, B.M.  
 J. Biol. Chem. 258, 12247-12251, 1983  
 A;Title: Conotoxin MI. Disulfide bonding and conformational states.  
 A;Reference number: A92396; PMID:84032400; PMID:6630187  
 C;Comment: This alpha-conotoxin, as an acetylcholine receptor inhibitor, is a postsynap  
 C;Superfamily: alpha-conotoxin  
 C;Keywords: acetylcholine receptor inhibitor; blocked carboxyl end; postsynaptic neurot  
 F.13/Modified site: blocked carboxyl end (Cys) (probably amidated) #status experimental

Query Match 21.1%; Score 26; DB 1; Length 13;  
 Best Local Similarity 44.4%; Pred. No. 2e+03;  
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 6 CLIPACRRN 14  
 |||||  
 Db 2 CCHPACGKH 10

RESULT 21  
 C21182  
 4K prothoracicotropic hormone III - silkworm (fragment)  
 C;Species: Bombyx mori (silkworm)  
 C;Date: 03-Aug-1990 #sequence\_revision 03-Aug-1990 #text\_change 12-Apr-1995  
 A;Accession: C21182  
 R;Nagasawa, H.; Kataoka, H.; Isogai, A.; Tamura, S.; Suzuki, A.; Ishizaki, H.; Mizoguch  
 Science 226, 1344-1345, 1984  
 A;Title: Amino-terminal amino acid sequence of the silkworm prothoracicotropic hormone  
 A;Reference number: A21182  
 A;Accession: C21182  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-19 <NAG>  
 C;Superfamily: insulin

Query Match 21.1%; Score 26; DB 2; Length 19;

Best Local Similarity 80.0%; Pred. No. 2.6e+03;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
5 CCLIP 9  
6 CCLQP 10

SULT 22  
1103  
at-stable enterotoxin ST-1a - Citrobacter freundii  
Species: Citrobacter freundii  
Date: 10-Nov-1992 #sequence\_revision 10-Nov-1992 #text\_change 18-Jun-1993  
Accession: A60103  
Quarino, A.; Giannella, R.; Thompson, M.R.  
fect. Immun. 57, 649-652, 1989  
Title: Citrobacter freundii produces an 18-amino-acid heat-stable enterotoxin identical  
Reference number: A60103; MUID:89108617; PMID:2912902  
Accession: A60103  
Molecule type: protein  
Residues: 1-18 <GUA>  
Superfamily: heat-stable enterotoxin ST

Query Match 20.7%; Score 25.5; DB 2; Length 18;  
Best Local Similarity 50.0%; Pred. No. 2.9e+03;  
Matches 5; Conservative 1; Mismatches 1; Indels 3; Gaps 1;  
5 CCLI---PAC 11  
5 CCELCNCPAC 14

SULT 23  
8953  
pha-conotoxin SI - cone shell (Conus striatus)  
Species: Conus striatus (striated cone)  
Date: 30-Jun-1989 #sequence\_revision 25-Apr-1997 #text\_change 23-May-1997  
Accession: A28953  
Zafaralla, G.C.; Ramilo, C.; Gray, W.R.; Karlstrom, R.; Olivera, B.M.; Cruz, L.J.  
chemistry 27, 7102-7105, 1988  
Title: Phylogenetic specificity of cholinergic ligands: alpha-conotoxin SI.  
Reference number: A28953; MUID:89062448; PMID:3196703  
Accession: A28953  
Molecule type: protein  
Residues: 1-13 <ZAP>  
Note: This sequence was confirmed by chemical synthesis  
Comment: This paralytic toxin from a fish-hunting cone snail inhibits the acetylcholin  
Superfamily: alpha-conotoxin  
Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neuro  
2-7,3-13/Disulfide bonds: #status experimental  
13/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 20.3%; Score 25; DB 2; Length 13;  
Best Local Similarity 66.7%; Pred. No. 2.7e+03;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
6 CLIPAC 11  
2 CCNPAC 7

SULT 24  
14823  
factory receptor I7 - mouse (fragment)  
Species: Mus musculus (house mouse)  
Date: 28-Apr-1995 #sequence\_revision 28-Apr-1995 #text\_change 17-Mar-1999  
Accession: A54823  
Chess, A.; Simon, I.; Cedar, H.; Axel, R.  
ll 78, 823-834, 1994  
Title: Allelic inactivation regulates olfactory receptor gene expression.  
Reference number: A54823; MUID:94373818; PMID:8087849  
Accession: A54823  
Status: Preliminary

A;Molecule type: DNA  
A;Residues: 1-8 <CHE>  
Query Match 19.5%; Score 24; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
12 RRNH 15  
3 RRNH 6

DB 3 RRNH 6

RESULT 25  
B54823  
olfactory receptor I7 - western wild mouse (fragment)  
C;Species: Mus spretus (western wild mouse)  
C;Date: 28-Apr-1995 #sequence\_revision 28-Apr-1995 #text\_change 17-Mar-1999  
C;Accession: B54823  
R;Chess, A.; Simon, I.; Cedar, H.; Axel, R.  
Cell 78, 823-834, 1994  
A;Title: Allelic inactivation regulates olfactory receptor gene expression.  
A;Reference number: A54823; MUID:94373818; PMID:8087849  
A;Accession: B54823  
A;Status: Preliminary  
A;Molecule type: DNA  
A;Residues: 1-8 <CHE>  
Query Match 19.5%; Score 24; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
12 RRNH 15  
3 RRNH 6

DB 3 RRNH 6

RESULT 26  
S61797  
T-cell-specific transcription factor 1 splice form F - human (fragment)  
N;Alternate names: transcription factor TCF-1F  
C;Species: Homo sapiens (man)  
C;Date: 19-Mar-1997 #sequence\_revision 18-Jul-1997 #text\_change 24-Jul-1998  
C;Accession: S61797; S61879  
R;Mayer, K.; Wolff, E.; Clevers, H.; Ballhausen, W.G.  
Biochim. Biophys. Acta 1263, 169-172, 1995  
A;Title: The human high mobility group (HMG)-box transcription factor TCF-1: novel isofo  
A;Reference number: S61796; MUID:95367594; PMID:7640309  
A;Accession: S61797  
A;Molecule type: mRNA  
A;Residues: 1-11 <WAY>  
A;Cross-references: EMBL:Z47363  
A;Note: DNA was also sequenced  
C;Keywords: alternative splicing; DNA binding; transcription factor  
Query Match 19.5%; Score 24; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.3e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
8 IPAC 11  
3 IPAC 6

DB 3 IPAC 6

RESULT 27  
A58700  
actgadinine [validated] - "Actinoplanes liguriae"  
N;Alternate names: gardimycin  
C;Species: "Actinoplanes liguriae"  
A;Note: ATCC 31048  
C;Date: 16-Jan-1998 #sequence\_revision 23-Jan-1998 #text\_change 15-Sep-2000  
C;Accession: A58700; A58701  
R;Zimmermann, N.; Jung, G.  
Eur. J. Biochem. 246, 809-819, 1997

Title: The three-dimensional solution structure of the lantibiotic murein-biosynthesis reference number: A58700; MUID:97363218; PMID:9219543  
 Accession: A58700  
 Molecule type: protein  
 Residues: 1-19 <ZIM>  
 Note: the assignment of residues 1-Ser and 6-Cys are based on model studies  
 Zimmermann, N.; Metzger, J.W.; Jung, G.  
 J. Biochem. 228, 786-797, 1995

Title: The tetracyclic lantibiotic actagardine. (1)H-NMR and (13)C-NMR assignments and reference number: A58701; MUID:95255286; PMID:7737178

Accession: A58701  
 Molecule type: protein  
 Residues: X', 2-5, X', 7-19 <Z12>  
 Note: residues 1 and 6, indicated as 'X', are serine and cysteine, but which is in which  
 Zimmermann, N.; Jung, G.  
 Submitted to the Brookhaven Protein Data Bank, May 1997

Reference number: A67976; PDB:1AJ1  
 Contents: annotation, conformation and cross-link assignments by (1)H- and (13)C-NMR.  
 Comment: The antibiotic activity arises through inhibition of a glycopeptide transglycosylase.  
 Superfamily: unassigned lantionine-containing peptides

Keywords: antibiotic; lantionine  
 1-6/Cross-link: sn-(2S,6R)-lantionine (Ser-Cys) #status experimental  
 7-12/Cross-link: (2S,3S,6R)-3-methyl-lanthionine (Thr-Cys) #status experimental  
 9-17/Cross-link: (2S,3S,6R)-3-methyl-lanthionine (Thr-Cys) #status experimental  
 14-19/Cross-link: (2S,3S,6R)-3-methyl-lanthionine (Thr-Cys) #status experimental

Query Match 19.5%; Score 24; DB 2; Length 19;  
 Best Local Similarity 44.4%; Pred. No. 4.9e+03;  
 Matches 4; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

3 WRCCIPAC 11  
 | | | |  
 4 WVCITIEC 12

SULT 28

3495  
 nopressin S - cone shell (Conus striatus)  
 Alternate names: Arg-vasopressin-S  
 Species: Conus striatus (striated cone)  
 Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 25-Apr-1997

Accession: B28495  
 Cruz, L.J.; de Santos, V.; Zafaralla, G.C.; Ramilo, C.A.; Zeikus, R.; Gray, W.R.; Oliver, J.  
 Biol. Chem. 262, 15821-15824, 1987

Title: Invertebrate vasopressin/oxytocin homologs. Characterization of peptides from C. Reference number: A92617; MUID:88058932; PMID:3680228

Accession: B28495  
 Molecule type: protein

Residues: 1-9 <CRU>  
 Superfamily: oxytocin-neurophysin  
 Keywords: amidated carboxyl end; venom  
 1-6/Disulfide bonds: #status experimental  
 9/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 18.7%; Score 23; DB 2; Length 9;  
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

6 CLIPACRR 13  
 | | | |  
 1 CTRNCP 8

SULT 29

6383  
 pothetical protein - soybean  
 Species: Glycine max (soybean)  
 Date: 30-Apr-1999 #sequence\_revision 30-Apr-1999 #text\_change 11-May-2000  
 Accession: T06383

Dewey, R.E.; Wilson, R.F.; Novitzky, W.P.; Goode, J.H.  
 Ant Cell 6, 1495-1507, 1994  
 Title: The AAP1 gene of soybean complements a cholinephosphotransferase-deficient mutant  
 Reference number: Z06169; MUID:95086383; PMID:7994181

A/Accession: T06383  
 A/Status: preliminary; translated from GB/EMBL/DDBJ  
 A/Molecule type: mRNA  
 A/Residues: 1-11 <DEW>  
 A/Cross-references: EMBL:U12735; NID:9530086; PIDN:AAA67718.1; PID:9530087  
 A/Experimental source: strain Dare; seed

Query Match 18.7%; Score 23; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 4.6e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 RCC 6  
 | | | |  
 Db 5 RCC 7

RESULT 30

B32800

hypotheoretical protein (P1 5' region) - human (fragment)

C/Species: Homo sapiens (man)  
 C/Date: 22-Nov-1989 #sequence\_revision 22-Nov-1989 #text\_change 30-Sep-1993

C/Accession: B32800  
 R/Jindal, S.; Dudani, A.K.; Singh, B.; Harley, C.B.; Gupta, R.S.

Mol. Cell. Biol. 9, 2279-2283, 1989

A/Title: Primary structure of a human mitochondrial protein homologous to the bacterial A/Reference number: A32800; MUID:89313783; PMID:2568584

A/Accession: B32800

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-15 <JIN>

A/Cross-references: GB:M22382

Query Match 18.7%; Score 23; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 5.8e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 ACRR 13  
 | | | |  
 Db 9 ACRR 12

RESULT 31

PC1324

hypotheoretical protein 19 - curled-leaved tobacco chloroplast (fragment)

C/Species: chloroplast Nicotiana glauca (curled-leaved tobacco)  
 C/Date: 03-May-1994 #sequence\_revision 07-Oct-1994 #text\_change 24-Feb-1995

C/Accession: PC1324

R/Pejes, E.; Engler, D.; Maliga, P.

Theor. Appl. Genet. 79, 28-32, 1990

A/Title: Extensive homologous chloroplast DNA recombination in the pt14 Nicotiana somat A/Reference number: PC1321

A/Accession: PC1324

A/Molecule type: DNA

A/Residues: 1-19 <FEJ>

C/Genetics:

A/Genome: chloroplast

C/Keywords: chloroplast

Query Match 18.7%; Score 23; DB 2; Length 19;  
 Best Local Similarity 50.0%; Pred. No. 6.8e+03;  
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 9 PACRRNHK 16  
 | | | | |  
 Db 1 FGRRRNYQ 8

RESULT 32

PC1322

hypotheoretical protein 19 - common tobacco chloroplast (fragment)

C/Species: chloroplast Nicotiana glauca (common tobacco)  
 C/Date: 03-May-1994 #sequence\_revision 07-Oct-1994 #text\_change 24-Feb-1995

C/Accession: PC1322



Fejes, E.; Engler, D.; Maliga, P.  
 Soc. Appl. Genet. 79, 28-32, 1990  
 Title: Extensive homologous chloroplast DNA recombination in the pt14 Nicotiana somati-  
 Reference number: PCI321  
 Accession: PCI322  
 Molecule type: DNA  
 Residues: 1-19 <FEJ>  
 Geneticks:  
 Genome: chloroplast  
 Keywords: chloroplast

Query Match 18.7%; Score 23; DB 2; Length 19;  
 Best Local Similarity 50.0%; Pred. No. 6.8e+03;  
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

9 PACRRNHK 16

1 PGRRRNYQ 8

SULT 33  
 S435  
 nganese peroxidase (EC 1.11.1.13) MnPI - Pleurotus eryngii (fragment)  
 Species: Pleurotus eryngii  
 Date: 19-Mar-1997 #sequence\_revision 29-Aug-1997 #text\_change 29-Aug-1997  
 Accession: S65435  
 Martinez, M.J.; Ruiz-Duenas, F.J.; Guillen, F.; Martinez, A.T.  
 x J. Biochem. 237, 424-432, 1996  
 Title: Purification and catalytic properties of two manganese peroxidase isoenzymes fr  
 Reference number: S65434; MUID:96215438; PMID:8647081

Accession: S65435  
 Molecule type: protein  
 Residues: 1-19 <MAR>  
 Experimental source: CBS 613.91  
 Keywords: manganese; oxidoreductase

Query Match 18.7%; Score 23; DB 2; Length 19;  
 Best Local Similarity 42.9%; Pred. No. 6.8e+03;  
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

2 NWRCCLI 8

11 NAACCVL 17

ISULT 34  
 37018  
 one Cfr protein - mouse (fragment)  
 Species: Mus sp. (mouse)  
 Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 28-Feb-1997  
 Accession: I57018  
 Dorin, J.K.; Stevenson, B.J.; Fleming, S.; Alton, E.W.; Dickinson, P.; Porteous, D.J.  
 Imm. Genome 5, 465-472, 1994  
 Title: Long-term survival of the exon 10 insertional cystic fibrosis mutant mouse is a  
 Reference number: I57018; MUID:95037043; PMID:7949729  
 Accession: I57018  
 Status: preliminary; translated from GB/EMBL/DBJ  
 Molecule type: DNA  
 Residues: 1-8 <RES>  
 Cross-references: GB:S74246; NID:g710482  
 Geneticks:  
 Gene: Cfr

Query Match 17.9%; Score 22; DB 2; Length 8;  
 Best Local Similarity 75.0%; Pred. No. 2.8e+05;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

9 PACR 12

5 PSOR 8

ISULT 35

I49637  
 deoxynucleotidyltransferase - mouse (fragment)  
 Species: Mus musculus (house mouse)  
 Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 05-Nov-1999  
 Accession: I49637  
 R.Koiwai, O.; Kaneda, T.; Morishita, R.  
 Biochem. Biophys. Res. Commun. 144, 185-190, 1987  
 Title: Analysis of human terminal deoxynucleotidyl transferase cDNA expressible in ma  
 Reference number: I45884; MUID:87213162; PMID:3579900  
 Accession: I49637  
 Status: preliminary; translated from GB/EMBL/DBJ  
 Molecule type: mRNA  
 Residues: 1-13 <RES>  
 Cross-references: GB:M26145; NID:g951208; PIDN:AAA74592.1; PID:g951209  
 Geneticks:  
 A:Gens: DNTT

Query Match 17.9%; Score 22; DB 2; Length 13;  
 Best Local Similarity 75.0%; Pred. No. 7.2e+03;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CLIP 9

Db 8 CLIP 11

Search completed: February 18, 2004, 06:29:21  
 Job time : 22 secs

result No.	Score	Query			DB	ID	Description
		Match	Length	Count			
1	123	100.0	19	1	CXR_CONTO	P59811	conus tulip
2	48	39.0	16	1	CXAÅ_CONPE	P59984	conus penna
3	44	35.8	16	1	CXA1_CONEP	P56638	conus episc
4	44	35.8	16	1	CXA2_CONPA	P56636	conus magus
5	42	34.1	16	1	CXAB_CONPE	P59985	conus penna
6	40	32.5	18	1	CXA1_CONER	P59982	conus ermin
7	38	30.9	16	1	CXA1_CONAL	P56639	conus aulic
8	37.5	30.5	14	1	CXA1_CONMA	P01521	conus magus
9	37	30.1	15	1	CXA3_CONAL	P56641	conus aulic
10	31	25.2	13	1	CXAÅ_CONST	P28878	conus stria
11	31	25.2	15	1	CXA1_CONGE	P01519	conus geogr
12	30	24.4	15	1	CXA2_CONAL	P56640	conus aulic
13	29.5	24.0	14	1	CXA1_CONCN	P56973	conus conso
14	28	22.8	12	1	CXA1_CONIM	P59983	conus imper
15	27	22.0	8	1	COM2_CONFU	P58785	conus putpu
16	27	22.0	18	1	HSTB_ECOLI	P01560	escherichia
17	26	21.1	9	1	DNF1_LOCHI	P16339	locusta mig
18	26	21.1	13	1	CXA2_CONGE	P01520	conus geogr
19	26	21.1	15	1	CX3B_CONQU	P58842	conus querc
20	25	20.3	17	1	CXMA_CONPE	P58926	conus penna
21	24	19.5	15	1	CX1B_CONBE	P58624	conus betul
22	24	19.5	15	1	CX3A_CONQU	P58841	conus querc
23	24	19.5	17	1	CXMB_CONPE	P58927	conus penna
24	24	19.5	19	1	LANA_ACTUG	P56850	actinoplan
25	24	19.5	19	1	LCRP_PETMA	Q10996	petromyzon
26	23	18.7	9	1	CONO_CONST	P05487	conus stria
27	23	18.7	12	1	CXL3_CONNR	P58809	conus marmo
28	23	18.7	18	1	LVC_ESTAC	P82175	estigmene a
29	22	17.9	10	1	GON2_CHEPR	P80578	chelyosoma
30	22	17.9	11	1	TIN1_HOPTI	P82651	hoplobatrac
31	22	17.9	15	1	AVP2_CAVPO	P83508	cavia porce
32	22	17.9	15	1	UC08_MAIZE	P80614	zea mays (m
33	22	17.1	19	1	OKYT_BUPRE	P42995	bufo regula

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1  CXAA_CONPE          STANDARD;          PRT;          16 AA.
2  P50984;
3  01-OCT-1996 (Rel. 34, Created)
4  01-OCT-1996 (Rel. 34, Last sequence update)
5  01-OCT-1996 (Rel. 34, Last sequence update)
6  28-FEB-2003 (Rel. 41, Last annotation update)
7  Alpha-conotoxin PnIA.
8  Conus pennaceus (Feathered cone).
9  Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
10 Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
11 Neogastropoda; Conoidea; Conidae; Conus.
12 NCBI_TaxID=37335;
13 [1]
14 SEQUENCE.
15 TISSUE=Venom;
16 MEDLINE=94347713; PubMed=8068627;
17 Fainzilber M., Hasson A., Oren R., Burlingame A.L., Gordon D.,
18 Spira M.E., Zlotkin E.;
19 "New mollusc-specific alpha-conotoxins block Aplysia neuronal
20 acetylcholine receptors.";
21 Biochemistry 33:9523-9529(1994).
22 [2]
23 SULFATION OF TYR-15.
24 MEDLINE=99242956; PubMed=10226369;
25 Wolfender J.L., Chu F., Ball H., Wolfender F., Fainzilber M.,
26 Baldwin M.A., Burlingame A.L.;
27 "Identification of tyrosine sulfation in Conus pennaceus conotoxins
28 alpha-PnIA and alpha-PnIB: further investigation of labile sulfo- and
29 phosphopeptides by electrospray, matrix-assisted laser desorption/ionization (MALDI) and atmospheric pressure MALDI mass
30 spectrometry.";
31 J. Mass Spectrom. 34:447-454(1999).
32 [3]
33 X-RAY CRYSTALLOGRAPHY (1.1 ANGSTROMS).
34 MEDLINE=96311277; PubMed=8740364;
35 Hu S.-H., Gehrmann J., Guddat L.W., Alewood P.F., Craik D.J.,
36 Martin J.L.;
37 "The 1.1 A crystal structure of the neuronal acetylcholine receptor
38 antagonist, alpha-conotoxin PnIA from Conus pennaceus.";
39 Structure 4:417-423(1996).
40 -!- FUNCTION: Alpha-conotoxins act on postsynaptic membranes, they
41 bind to the nicotinic acetylcholine receptors (nAChR) and thus
42 inhibit them. In contrast to other alpha-conotoxins, which are
43 selective for vertebrate skeletal muscle nAChR, the Conus
44 pennaceus alpha-conotoxins block nAChR in mollusks.
45 -!- SUBCELLULAR LOCATION: Secreted.
46 -!- TISSUE SPECIFICITY: Expressed by the venom duct.
47 -!- SIMILARITY: Belongs to the conotoxin A-superfamily. Alpha-type
48 family.
49 PIR; A54877; A54877.
50 PDB; 1PEN; 21-APR-97.
51 Postsynaptic neurotoxin; Neurotoxin; Toxin;
52 Acetylcholine receptor inhibitor; Amidation; Sulfation; 3D-structure.
53 DISULFID 2 8
54 T MOD_RES 3 16 SULFATION.
55 T MOD_RES 15 15 AMIDATION.
56 T MOD_RES 16 16
57 T HELIX 2 4
58 T HELIX 6 11
59 T TURN 13 16
60 Q SEQUENCE 16 AA; 1628 MW; 05310FF95EC99005 CRC64;
61 Query Match 39.0%; Score 48; DB 1; Length 16;
62 Best Local Similarity 40.0%; Pred. No. 0.26;
63 Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
64
65 Y 5 CCLIPACRRNHKKFC 19
66 ||| ||| ||| :
67 2 CGLSPPCAANNPDYC 16
68
69 RESULT 3
70 XAL_CONEP          STANDARD;          PRT;          16 AA.
71 D  CXAL_CONEP

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AC P56638;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Alpha-conotoxin Epi.
OS Conus episcopatus (Bishop's cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=88764;
RN [1]
RP X-RAY CRYSTALLOGRAPHY (1.1 ANGSTROMS).
RX MEDLINE=98376423; PubMed=9708977;
RA Hu S.H., Loughnan M., Miller R., Weeks C.M., Blessing R.H.,
RA Alewood P.F., Lewis R.J., Martin J.L.;
RT "The 1.1-A resolution crystal structure of [Tyr15]Epi, a novel
RL alpha-conotoxin from Conus episcopatus, solved by direct methods.";
RL Biochemistry 37:11425-11433(1998).
CC -!- FUNCTION: Alpha-conotoxins act on postsynaptic membranes, they
CC bind to the nicotinic acetylcholine receptors (nAChR) and thus
CC inhibit them. This peptide blocks mammalian nicotinic
CC acetylcholine receptors composed of alpha-3/beta-2 and alpha-
CC 3/beta-4 subunits.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -!- SIMILARITY: Belongs to the conotoxin A-superfamily. Alpha-type
CC family.
CC PIR; A59042; A59042.
CC PDB; 1AOM; 13-JAN-99.
CC Postsynaptic neurotoxin; Neurotoxin; Toxin;
CC Acetylcholine receptor inhibitor; Amidation;
CC Sulfation; 3D-structure.
KW DISULFID 2 8
FT DISULFID 3 16
FT MOD_RES 15 15 SULFATION.
FT MOD_RES 16 16 AMIDATION.
FT HELIX 2 4
FT HELIX 6 11
FT TURN 13 16
SQ SEQUENCE 16 AA; 1792 MW; C63385F376C99BAC CRC64;
Query Match 35.8%; Score 44; DB 1; Length 16;
Best Local Similarity 40.0%; Pred. No. 1;
Matches 6; Conservative 2; Mismatches 7; Indels 0; Gaps 0;
OY 5 CCLIPACRRNHKKFC 19
DB ||| ||| ||| :
2 CGLSPPCAANNPDYC 16

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RESULT 4
CXAA2_CONWA          STANDARD;          PRT;          16 AA.
ID CXAA2_CONWA
AC P56636;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Alpha-conotoxin MII (M2).
OS Conus magus (Magus cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=6492;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Venom;
RX MEDLINE=96205934; PubMed=8631783;
RA Cartier G.E., Yoshikami D., Gray W.R., Luo S., Olivera B.M.,
RA McIntosh J.M.;
RT "A new alpha-conotoxin which targets alpha3beta2 nicotinic
RT acetylcholine receptors.";
RL J. Biol. Chem. 271:7522-7528(1996).
RN [2]

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-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Expressed by the venom duct.
-!- MASS SPECTROMETRY: MW=1667.6; METHOD=Electrospray.
-!- SIMILARITY: Belongs to the conotoxin A-superfamily. Alpha-type family.
PIR: CS9045; CS9045.
HSPSP; P50984; 1PEN.
Postsynaptic neurotoxin; Neurotoxin; Toxin;
Acetylcholine receptor inhibitor; Amidation.
DISULFID 2 8
DISULFID 3 16
MOD_RES 16 16
SEQUENCE 16 AA; 1673 MW; 1E310D3B9DFD7001 CRC64;
Query Match 30.1%; Score 37; DB 1; Length 16;
Best Local Similarity 33.3%; Pred. No. 11;
Matches 5; Conservative 2; Mismatches 8; Indels 0; Gaps 0;
5 CCLIPACRRNHKKFC 19
||| | | | | | | | | | | | | | |
2 CCSYPFCFATNSGYC 16

SULT 10
AA_CONST STANDARD; PRT; 13 AA.
P28878;
01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Alpha-conotoxin SIA (SIA).
Conus striatus (Striated cone).
Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
NCBI_TaxID=6493;
[1]
SEQUENCE.
TISSUE=Venom;
MEDLINE=91369955; PubMed=1892838;
Myers R.A., Zafarella G.C., Gray W.R., Abbot J., Cruz L.J.,
Olivera B.M.;
"Alpha-conotoxins, small peptide probes of nicotinic acetylcholine receptors.";
Biochemistry 30:9370-9377(1991).
-!- FUNCTION: Alpha-conotoxins act on postsynaptic membranes, they bind to the nicotinic acetylcholine receptors (nAChR) and thus inhibit them.
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Expressed by the venom duct.
-!- SIMILARITY: Belongs to the conotoxin A-superfamily. Alpha-type family.
PIR: A40312; NTKNAS.
Postsynaptic neurotoxin; Neurotoxin; Toxin;
Acetylcholine receptor inhibitor; Amidation.
DISULFID 2 7
DISULFID 3 13
MOD_RES 13 13
SEQUENCE 13 AA; 1461 MW; DEF1931982457EBD CRC64;
Query Match 25.2%; Score 31; DB 1; Length 13;
Best Local Similarity 55.6%; Pred. No. 70;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
6 CCLIPACRRN 14
||| | | | | | | | | | | | |
2 CCHPACGCKN 10

RESULT 11
CAL_CONGE STANDARD; PRT; 15 AA.
; CXAI_CONGE
; P01519;

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DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Alpha-conotoxin GIA [Contains: Alpha-conotoxin GI (GI)].
OS Conus geographus (Geography cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
CX NCBI_TaxID=6491;
RN [1]
RP SEQUENCE.
RX MEDLINE=81191854; PubMed=7014556;
RA Gray W.R., Lucue F.A., Olivera B.M., Barrett J., Cruz L.J.;
RT "Peptide toxins from Conus geographus venom.";
RN [2]
RX MEDLINE=83105694; PubMed=7152021;
RA Nishiuchi Y., Sakakibara S.;
RT "Primary and secondary structure of conotoxin GI, a neurotoxic tridecapeptide from a marine snail.";
RN [3]
RX MEDLINE=84280842; PubMed=6466616;
RA Gray W.R., Lucue F.A., Galyean R., Atherton E., Sheppard R.C.,
RA Stone B.L., Reyes A., Alford J., McIntosh M., Olivera B.M.,
RA Cruz L.J., Rivier J.;
RT "Conotoxin GI: disulfide bridges, synthesis, and preparation of iodinated derivatives.";
RN [4]
RX MEDLINE=95034849; PubMed=7947815;
RA Hann R.M., Pagan O.R., Sterovic V.A.;
RT "The alpha-conotoxins GI and MI distinguish between the nicotinic acetylcholine receptor agonist sites while SI does not.";
RN [5]
RX MEDLINE=95349531; PubMed=7623764;
RA Greebe D.R., Dumm J.M., Levitan E.S., Abramson S.N.;
RT "alpha-Conotoxins selectively inhibit one of the two acetylcholine binding sites of nicotinic receptors.";
RN [6]
RX MEDLINE=97317090; PubMed=9174364;
RA Greebe D.R., Gray W.R., Abramson S.N.;
RT "Determinants involved in the affinity of alpha-conotoxins GI and SI for the muscle subtype of nicotinic acetylcholine receptors.";
RN [7]
RX MEDLINE=96378624; PubMed=8784187;
RA Guddat L.W., Martin J.A., Shan L., Edmundson A.B., Gray W.R.;
RT "Three-dimensional structure of the alpha-conotoxin GI at 1.2-A resolution.";
RN [8]
RX MEDLINE=89352562; PubMed=2765514;
RA Kobayashi Y., Ohkubo T., Kyogoku Y., Nishiuchi Y., Sakakibara S.,
RA Braun W., Go N.;
RT "Solution conformation of conotoxin GI determined by 1H nuclear magnetic resonance spectroscopy and distance geometry calculations.";
RN [9]
RX MEDLINE=89375269; PubMed=2775719;
RA Pardi A., Galdes A., Florence J., Maniconte D.;
RT "Solution structures of alpha-conotoxin GI determined by two-

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dimensional NMR spectroscopy. ";  
 Biochemistry 28:5494-5501(1989).  
 [10]  
 STRUCTURE BY NMR OF GI.  
 MEDLINE=98321613; PubMed=9660176;  
 Maslennikov I.V., Sobol A.G., Gladky K.V., Lugovskoy A.A.,  
 Ostrovsky A.G., Tsetlin V.I., Ivanov V.T., Arseniev A.S.;  
 "Two distinct structures of alpha-conotoxin GI in aqueous solution. ";  
 Eur. J. Biochem. 254:238-247(1998).  
 [11]  
 STRUCTURE BY NMR OF GI.  
 MEDLINE=98239743; PubMed=9571060;  
 Gehrmann J., Alewood P.F., Craik  
 "Structure determination of the three disulfide bond isomers of  
 alpha-conotoxin GI: a model for the role of disulfide bonds in  
 structural stability. ";  
 J. Mol. Biol. 278:401-415(1998).  
 [12]  
 STRUCTURE BY NMR OF AN ANTITOXIC ANALOG OF GI.  
 MEDLINE=99438341; PubMed=10508392;  
 Mok K.H., Han K.H.;  
 "NMR solution conformation of an antitoxic analogue of alpha-conotoxin  
 GI: identification of a common nicotinic acetylcholine receptor  
 alpha(1)-subunit binding surface for small ligands and alpha-  
 conotoxins. ";  
 Biochemistry 38:11895-11904(1999).  
 -!- FUNCTION: Alpha-conotoxins act on postsynaptic membranes, they  
 bind to the nicotinic acetylcholine receptors (nAChR) and thus  
 inhibit them. The higher affinity site for alpha-conotoxin GI is  
 the alpha/delta site on mouse muscle-derived BC3H-1 receptor, and  
 the other site (alpha/gamma site) on nicotinic receptors from  
 Torpedo californica electric organ.  
 -!- SUBCELLULAR LOCATION: Secreted.  
 -!- TISSUE SPECIFICITY: Expressed by the venom duct.  
 -!- SIMILARITY: Belongs to the conotoxin A-superfamily. Alpha-type  
 family.  
 PIR; A01782; NTKNAG.  
 PDB; 1NOT; 07-DEC-96.  
 PDB; 1XGA; 16-FEB-99.  
 PDB; 1XGB; 16-FEB-99.  
 PDB; 1XGC; 23-MAR-99.  
 PDB; 1Q83; 06-OCT-99.  
 W Acetylcholine receptor inhibitor; Neurotoxin; Toxin;  
 Postsynaptic neurotoxin; Amidation; 3D-structure.  
 T PEPTIDE 1 15 ALPHA-CONOTOXIN GIA.  
 T PEPTIDE 2 7 ALPHA-CONOTOXIN GI.  
 T DISULFID 3 13  
 T MOD\_RES 13 13  
 T AMIDATION (G-14 PROVIDE AMIDE GROUP) (IN  
 T ALPHA-CONOTOXIN GI).  
 T AMIDATION (IN ALPHA-CONOTOXIN GIA).  
 T R->A: REDUCTION IN AFFINITY FOR BOTH  
 T ALPHA/DELTA AND ALPHA/GAMMA SITES ON  
 T BC3H-1 RECEPTORS AND LOSS OF AFFINITY FOR  
 T BOTH ALPHA/DELTA AND ALPHA/GAMMA SITES ON  
 T TORPEDO RECEPTORS (IN GI).  
 T STRAND 2 2  
 T HELIX 5 10  
 T STRAND 12 12  
 T SEQUENCE 15 AA; 1628 MW; 2AE73EE90F8C2E19 CRC64;  
 Query Match 25.2%; Score 31; DB 1; Length 15;  
 Best Local Similarity 50.0%; Pred. No. 80;  
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
 Y 6 CLIPACRNH 15  
 | | | | |  
 b 2 CCNPACGRHY 11  
 | | | | |  
 RESULT 12  
 XA2\_CONAL STANDARD; PRT; 15 AA.  
 D -CXA2\_CONAL

P56640;  
 15-DEC-1998 (Rel. 37, Created)  
 15-DEC-1998 (Rel. 37, Last sequence update)  
 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Alpha-conotoxin AUIB.  
 OS Conus aulicus (Court cone).  
 OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypogastropoda;  
 OC Neogastropoda; Conoidea; Conidae; Conus.  
 OC NCBI\_TaxID=89437;  
 RN [1]  
 RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.  
 RC Tissue-Venom;  
 RX MEDLINE=99003392; PubMed=9786965;  
 RA Luo S., Kulak J.M., Cartier G.E., Jacobsen R.B., Yoshikami D.,  
 Olivera B.M., McIntosh J.M.;  
 "Alpha-conotoxin AUIB selectively blocks alpha3 beta4 nicotinic  
 acetylcholine receptors and nicotine-evoked norepinephrine release. ";  
 J. Neurosci. 18:8571-8579(1998).  
 RN [2]  
 RP STRUCTURE BY NMR.  
 RX MEDLINE=20187595; PubMed=10722709;  
 RA Cho J.H., Mok K.H., Olivera B.M., McIntosh J.M., Park K.H., Han K.H.;  
 "Nuclear magnetic resonance solution conformation of alpha-conotoxin  
 AUIB, an alpha(3)beta(4) subtype-selective neuronal nicotinic  
 acetylcholine receptor antagonist. ";  
 J. Biol. Chem. 275:8680-8685(2000).  
 RN [3]  
 RP STRUCTURE BY NMR.  
 RX MEDLINE=22359066; PubMed=12376538;  
 RA Dutton J.L., Bansal P.S., Hogg R.C., Adams D.J., Alewood P.F.,  
 Craik D.J.;  
 "A new level of conotoxin diversity, a non-native disulfide bond  
 connectivity in alpha-conotoxin AUIB reduces structural definition  
 but increases biological activity. ";  
 J. Biol. Chem. 277:48849-48857(2002).  
 CC -!- FUNCTION: Alpha-conotoxins act on postsynaptic membranes, they  
 bind to the nicotinic acetylcholine receptors (nAChR) and thus  
 inhibit them. This peptide blocks mammalian nicotinic  
 acetylcholine receptors composed of alpha-3/beta-4 subunits.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.  
 CC -!- MASS SPECTROMETRY: MW=1572.5; METHOD=Electrospray.  
 CC -!- SIMILARITY: Belongs to the conotoxin A-superfamily. Alpha-type  
 family.  
 CC PDB; 1DG2; 23-MAY-00.  
 CC PDB; 1MXN; 30-DEC-02.  
 CC PDB; 1MXP; 30-DEC-02.  
 KW Postsynaptic neurotoxin; Neurotoxin; Toxin;  
 FT Acetylcholine receptor inhibitor; Amidation; 3D-structure.  
 FT DISULFID 2 8  
 FT DISULFID 3 15  
 FT MOD\_RES 15 15 AMIDATION.  
 FT SEQUENCE 15 AA; 1578 MW; 84EFE95FDC700155 CRC64;  
 Query Match 24.4%; Score 30; DB 1; Length 15;  
 Best Local Similarity 57.1%; Pred. No. 11e+02;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 5 CCLIPAC 11  
 | | | | |  
 Db 2 CCSYPPC 8  
 | | | | |  
 RESULT 13  
 CXA1\_CONCN STANDARD; PRT; 14 AA.  
 ID CXA1\_CONCN  
 AC P56973;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Alpha-conotoxin CnIB [Contains: Alpha-conotoxin CnIB].  
 OS Conus consors (Singed cone).

Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;  
 Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;  
 Neogastropoda; Conoidea; Conidae; Conus.  
 NCBI\_TaxID=101297;  
 [1]  
 SEQUENCE, SYNTHESIS, CHARACTERIZATION, AND STRUCTURE BY NMR.  
 TISSUE=Venom;  
 MEDLINE=92255390; PubMed=10320362;  
 Favreau P., Kriem I., le Gall F., Bobenrieth M.J., Lamthanh H.,  
 Bouet F., Servent D., Molgo J., Menez A., Letourneux Y.,  
 Lancelin J.-M.;  
 "Biochemical characterization and nuclear magnetic resonance  
 structure of novel alpha-conotoxins isolated from the venom of Conus  
 consors";  
 Biochemistry 38:6317-6326(1999).  
 -!- FUNCTION: Alpha-conotoxins act on postsynaptic membranes, they  
 bind to the nicotinic acetylcholine receptors (nAChR) and thus  
 inhibit them. This peptide seems to be a potent and selective  
 blocker of muscular subtype of nAChR.  
 -!- SUBCELLULAR LOCATION: Secreted.  
 -!- TISSUE SPECIFICITY: Expressed by the venom duct.  
 -!- SIMILARITY: Belongs to the conotoxin A-superfamily. Alpha-type  
 family.  
 PIR; A58963; A58963.  
 PDB; 1B45; 09-JUL-99.  
 Postsynaptic neurotoxin; Neurotoxin; Toxin;  
 Acetylcholine receptor inhibitor; Amidation; 3D-structure.  
 PEPTIDE 1 14  
 14 ALPHA-CONOTOXIN CNIA.  
 PEPTIDE 3 14  
 8 ALPHA-CONOTOXIN CNIB.  
 DISULFID 3 8  
 4 14  
 MOD RES 14 14  
 14 14  
 HELIX 6 8  
 5 10  
 TURN 9 10  
 SEQUENCE 14 AA; 1548 MW; DEEE1969BF5E5BD CRC64;  
 Query Match 24.0%; Score 29.5; DB 1; Length 14;  
 Best Local Similarity 75.0%; Pred. No. 1.2e-02;  
 Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;  
 4 RCCLIPAC 11  
 |||||  
 2 RCC-HPAC 8  
 SULT 14  
 AL CONIM STANDARD; PRT; 12 AA.  
 PS0983;  
 01-OCT-1996 (Rel. 34, Created)  
 01-OCT-1996 (Rel. 34, Last sequence update)  
 28-FEB-2003 (Rel. 41, Last annotation update)  
 Alpha-conotoxin Imi.  
 Conus imperialis (Imperial cone).  
 Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;  
 Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;  
 Neogastropoda; Conoidea; Conidae; Conus.  
 NCBI\_TaxID=35631;  
 [1]  
 SEQUENCE, AND SYNTHESIS.  
 TISSUE=Venom;  
 MEDLINE=94266889; PubMed=8206995;  
 McIntosh J.M., Yoshikami D., Mahe E., Nielsen D.B., Rivier J.E.,  
 Gray W.R., Olivera B.M.;  
 "A nicotinic acetylcholine receptor ligand of unique specificity,  
 alpha-conotoxin Imi";  
 J. Biol. Chem. 269:16733-16739(1994).  
 [2]  
 CHARACTERIZATION  
 MEDLINE=95379776; PubMed=7651351;  
 Jonsson D.S., Martinez J., Elgoyhen A.B., Heinemann S.F.,  
 McIntosh J.M.;  
 "Alpha-conotoxin Imi exhibits subtype-specific nicotinic

RT acetylcholine receptor blockade: preferential inhibition of homomeric  
 RT alpha 7 and alpha 9 receptors.";  
 RL Mol. Pharmacol. 48:194-199(1995).  
 RN [3]  
 RN STRUCTURE BY NMR.  
 RX MEDLINE=99212205; PubMed=10194298;  
 RA Rogers J.P., Luginbuhl P., Shen G.S., McCabe R.T., Stevens R.C.,  
 RA Wemmer D.E.;  
 "NMR solution structure of alpha-conotoxin Imi and comparison to  
 RT other conotoxins specific for neuronal nicotinic acetylcholine  
 RT receptors";  
 RL Biochemistry 38:3874-3882(1999).  
 RN [4]  
 RN STRUCTURE BY NMR.  
 RX MEDLINE=99280313; PubMed=10350614;  
 RA Gouda H., Hirono S.;  
 RT "Solution structure of alpha-conotoxin Imi determined by  
 RT two-dimensional NMR spectroscopy";  
 RL Biochim. Biophys. Acta 1431:384-394(1999).  
 RN [5]  
 RN STRUCTURE BY NMR.  
 RX MEDLINE=99158061; PubMed=10050774;  
 RA Maslemnikov I.V., Shenkarev Z.O., Zhmak M.N., Ivanov V.T.,  
 RA Methfessel C., Tsetlin V.I., Arseniev A.S.;  
 RT "NMR spatial structure of alpha-conotoxin Imi reveals a common  
 RT scaffold in snail and snake toxins recognizing neuronal nicotinic  
 RT acetylcholine receptors";  
 RL FEBS Lett. 444:275-280(1999).  
 RN [6]  
 RN STRUCTURE BY NMR.  
 RX MEDLINE=99358772; PubMed=10431825;  
 RA Lamthanh H., Jegou-Matheron C., Servent D., Menez A., Lancelin J.-M.;  
 RT "Minimal conformation of the alpha-conotoxin Imi for the alpha7  
 RT neuronal nicotinic acetylcholine receptor recognition: correlated CD,  
 RT NMR and binding studies";  
 RL FEBS Lett. 454:293-298(1999).  
 RN [7]  
 RN STRUCTURE BY NMR.  
 RX MEDLINE=99324017; PubMed=10395477;  
 RA Gehrmann J., Daly N.L., Alewood P.F., Craik D.J.;  
 RT "Solution structure of alpha-conotoxin Imi by 1H nuclear magnetic  
 RT resonance";  
 RL J. Med. Chem. 42:2364-2372(1999).  
 RN [8]  
 RN MUTAGENESIS OF ASP-5; ARG-7 AND ARG-11, AND STRUCTURE BY NMR OF THESE  
 RN THREE MUTANTS.  
 RX MEDLINE=20574023; PubMed=11124036;  
 RA Rogers J.P., Luginbuhl P., Pemberton K., Harty P., Wemmer D.E.,  
 RA Stevens R.C.;  
 RT "Structure-activity relationships in a peptidic alpha7 nicotinic  
 RT acetylcholine receptor antagonist";  
 RL J. Mol. Biol. 304:911-926(2000).  
 CC -!- FUNCTION: Alpha-conotoxins act on postsynaptic membranes, they  
 CC bind to the nicotinic acetylcholine receptors (nAChR) and thus  
 CC inhibit them. It is highly active against the neuromuscular  
 CC receptor in frog but not in mice. In contrast, it induces seizures  
 CC when injected centrally in mice and rats. It targets neuronal  
 CC nAChRs in mammals. It blocks homomeric alpha-7 nicotinic receptors  
 CC with the highest apparent affinity and homomeric alpha-9 receptors  
 CC with 8-fold lower affinity. It has no effect on receptors composed  
 CC of alpha-2/beta-2, alpha-3/beta-2, alpha-4/beta-2, alpha-2/beta-4,  
 CC alpha-3/beta-4, or alpha-4/beta-4 subunit combinations.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.  
 CC -!- SIMILARITY: Belongs to the conotoxin A-superfamily. Alpha-type  
 CC family.  
 DR PIR; A53709; A53709.  
 DR PDB; 1CNL; 27-MAY-99.  
 DR PDB; 1E74; 27-DEC-00.  
 DR PDB; 1E75; 27-DEC-00.  
 DR PDB; 1E76; 27-DEC-00.  
 DR PDB; 1G2G; 08-NOV-00.  
 DR PDB; 1IM1; 15-JUN-99.



PDB: 1IML; 23-APR-99.  
 Postsynaptic neurotoxin; Neurotoxin; Toxin;  
 Acetylcholine receptor inhibitor; Amidation; 3D-structure.  
 DISULFID 2 8  
 MOD RES 3 12  
 AMIDATION.  
 D->L: REDUCTION OF TOXICITY.  
 MUTAGEN 5 5  
 R->L: REDUCTION OF TOXICITY.  
 MUTAGEN 7 7  
 R->E: NO LOSS OF ACTIVITY.  
 MUTAGEN 11 11  
 HELIX 2 4  
 TURN 6 8  
 TURN 10 12  
 SEQUENCE 12 AA; 1357 MW; 9C29CEA545A4176A CRC64;

Query Match 22.8%; Score 28; DB 1; Length 12;  
 Best Local Similarity 57.1%; Pred. NO. 1.8e+02;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

5 CCLIPAC 11  
 2 CCSDPRC 8

RESULT 15  
 W2\_CONPU STANDARD; PRT; 8 AA.  
 P58785;  
 28-FEB-2003 (Rel. 41, Created)  
 28-FEB-2003 (Rel. 41, Last sequence update)  
 28-FEB-2003 (Rel. 41, Last annotation update)  
 Leu-contryphan-P.  
 Conus purpurascens (Purple cone).  
 Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;  
 Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;  
 Neogastropoda; Conoidea; Conidae; Conus.  
 NCBI\_TaxID=411690;

SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.  
 STRAIN=Clipperton Island; TISSUE=Venom;  
 MEDLINE=9338839; PubMed=10461743;  
 Jacobsen R.B., Jimenez E.C., De la Cruz R.G.C., Gray W.R., Cruz L.J.,  
 Olivera B.M.;  
 "A novel D-leucine-containing Conus peptide: diverse conformational  
 dynamics in the contryphan family.";  
 J. Pept. Res. 54:93-99(1999).  
 -!- SUBCELLULAR LOCATION: Secreted.  
 -!- TISSUE SPECIFICITY: Expressed by the venom duct.  
 -!- MASS SPECTROMETRY: MW=886.4; METHOD=LSIMS.  
 Toxin; Hydroxylation; D-amino acid.  
 DISULFID 2 4  
 MOD RES 4 4  
 SEQUENCE 8 AA; 890 MW; 75A367672732CEB8 CRC64;

Query Match 22.0%; Score 27; DB 1; Length 8;  
 Best Local Similarity 57.1%; Pred. NO. 1.4e+05;  
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

5 CCLIPAC 11  
 2 CVLLPWC 8

RESULT 16  
 STB\_ECOLI STANDARD; PRT; 16 AA.  
 HSTB\_ECOLI  
 P01560;  
 21-JUL-1986 (Rel. 01, Created)  
 21-JUL-1986 (Rel. 01, Last sequence update)  
 28-FEB-2003 (Rel. 41, Last annotation update)  
 Heat-stable enterotoxin ST-2 (ST-B).  
 Escherichia coli.  
 Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

OC Enterobacteriaceae; Escherichia.  
 OX NCBI\_TaxID=562;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=O42:K86:H37 / 18D;  
 RX MEDLINE=81264141; PubMed=7021541;  
 RA Chan S.-K., Giannelis R.A.;  
 RT "Amino acid sequence of heat-stable enterotoxin produced by  
 Escherichia coli pathogenic for man.";  
 RL J. Biol. Chem. 256:7744-7746(1981).  
 RN [2]  
 RP DISULFIDE BONDS.  
 RX MEDLINE=87191003; PubMed=3552731;  
 RA Shimonishi Y., Hidaka Y., Koizumi M., Hane M., Aimoto S., Takeda T.,  
 Miwatani T., Takeda Y.;  
 RT "Mode of disulfide bond formation of a heat-stable enterotoxin (STh)  
 produced by a human strain of enterotoxigenic Escherichia coli.";  
 RL FEBS Lett. 215:165-170(1987).  
 CC -!- FUNCTION: TOXIN WHICH ACTIVATES THE PARTICULATE FORM OF GUANYLATE  
 CYCLASE AND INCREASES CYCLIC GMP LEVELS WITHIN THE HOST  
 INTESTINAL EPITHELIAL CELLS.  
 CC -!- DISEASE: BOTH HEAT-STABLE AND HEAT-LABILE ENTEROTOXINS ARE  
 PRODUCED BY PATHOGENIC STRAINS OF E. COLI AND AFFECT THE DIGESTIVE  
 TRACT OF MAMMALS.  
 CC -!- SIMILARITY: Belongs to the heat-stable enterotoxin family.  
 DR PIR; A01823; OHEC2.  
 DR HSP; P01559; 1ETN.  
 DR InterPro; IPR001489; Enterotoxin\_HS.  
 DR Pfam; PF02048; Enterotoxin\_HS; 1.  
 DR PROSITE; PS00273; ENTEROTOXIN\_H\_STABLE; 1.  
 DR Toxin; Enterotoxin.  
 FT DISULFID 5 10  
 FT DISULFID 6 14  
 FT DISULFID 9 17  
 SQ SEQUENCE 18 AA; 1978 MW; D0C975F49D500650 CRC64;

Query Match 22.0%; Score 27; DB 1; Length 18;  
 Best Local Similarity 66.7%; Pred. NO. 3.7e+02;  
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 CLIPAC 11  
 Db 9 CCYPAC 14

RESULT 17  
 DNFL\_LOCMI STANDARD; PRT; 9 AA.  
 ID DNFL\_LOCMI  
 AC P16339;  
 DT 01-AUG-1990 (Rel. 15, Created)  
 DT 01-AUG-1990 (Rel. 15, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Locupressin (Diuretic neuropeptide F1/F2).  
 OS Locusta migratoria (Migratory locust).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;  
 OC Acridoidea; Acrididae; Oedipodinae; Locusta.  
 OX NCBI\_TaxID=7004;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Suboesophageal ganglion, and Thoracic ganglion;  
 RX MEDLINE=8807707; PubMed=3689410;  
 RA Proulx J.P., Miller C.A., Li J.P., Carney R.L., Girardie A.,  
 Delage M., Schooley D.A.;  
 RT "Identification of an arginine vasopressin-like diuretic hormone from  
 Locusta migratoria.";  
 RL Biochem. Biophys. Res. Commun. 149:180-186(1987).  
 CC -!- FUNCTION: DIURETIC HORMONE.  
 CC -!- SUBUNIT: Monomer (F1) and homodimer (F2); disulfide-linked.  
 CC -!- SIMILARITY: Belongs to the vasopressin/oxytocin family.  
 DR PIR; A29477; A29477.  
 DR InterPro; IPR000981; Neuhyp\_horm.  
 DR Pfam; PF00220; hormone4; 1.

PROSITE; PS00264; NEUROHYPOPHYS\_HORM; 1.  
Hormone; Neuropeptide; Amidation.  
DISULFID 1 6 IN FL.  
INTERCHAIN (WITH C-6) (IN F2).  
INTERCHAIN (WITH C-1) (IN F2).  
AMIDATION.  
MOD\_RES 9 9  
SEQUENCE 9 AA; 976 MW; 56EB176EB451A057 CRC64;  
Query Match 21.1%; Score 26; DB 1; Length 9;  
Best Local Similarity 62.5%; Pred. No. 1.4e+05;  
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
6 CLIPACRR 13  
|||||  
1 CLITNCP 8  
SULT 18  
A2 CONGE STANDARD; PRT; 13 AA.  
P01520;  
21-JUL-1986 (Rel. 01, Created)  
21-JUL-1986 (Rel. 01, Last sequence update)  
28-FEB-2003 (Rel. 41, Last annotation update)  
Alpha-conotoxin GII.  
Conus geographus (Geography cone).  
Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;  
Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;  
Neogastropoda; Conoidea; Conidae; Conus.  
NCBI\_TaxID=6491;  
[1]  
SEQUENCE.  
MEDLINE=81191854; PubMed=7014556;  
Gray W.R., Luque A., Olivera B.M., Barrett J., Cruz L.J.;  
"Peptide toxins from Conus geographus venom.";  
J. Biol. Chem. 256:4734-4740(1981).  
[2]  
DISULFIDE BONDS  
MEDLINE=84280842; PubMed=6466616;  
Gray W.R., Luque F.A., Galyean R., Atherton E., Sheppard R.C.,  
Stone B.L., Reyes A., Alford J., McIntosh M., Olivera B.M.,  
Cruz L.J., Rivier J.;  
"Conotoxin GI: disulfide bridges, synthesis, and preparation of  
iodinated derivatives";  
Biochemistry 23:2796-2802(1984).  
bind to the nicotinic acetylcholine receptors (nAChR) and thus  
inhibit them.  
-!- TISSUE SPECIFICITY: Expressed by the venom duct.  
-!- SIMILARITY: Belongs to the conotoxin A-superfamily. Alpha-type  
family.  
PIR; A01783; NTKN2G.  
HSSP; P56973; 1845.  
Postsynaptic neurotoxin; Neurotoxin; Toxin;  
Acetylcholine receptor inhibitor; Amidation.  
DISULFID 2 7  
DISULFID 3 13  
MOD\_RES 13 13  
SEQUENCE 13 AA; 1422 MW; DEEB831C3297EBD CRC64;  
Query Match 21.1%; Score 26; DB 1; Length 13;  
Best Local Similarity 44.4%; Pred. No. 3.8e+02;  
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
6 CLIPACRR 14  
|||||  
2 CCHPACGR 10  
RESULT 19  
X3B\_CONQU STANDARD; PRT; 15 AA.  
D\_CX3B\_CONQU

P58842;  
28-FEB-2003 (Rel. 41, Created)  
28-FEB-2003 (Rel. 41, Last sequence update)  
28-FEB-2003 (Rel. 41, Last annotation update)  
Conotoxin QcIIIB.  
Conus quercinus (Oak cone).  
Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;  
Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;  
Neogastropoda; Conoidea; Conidae; Conus.  
NCBI\_TaxID=101313;  
[1]  
SEQUENCE.  
MEDLINE=90327072; PubMed=2165278;  
Abogadie F.C., Ramilo C.A., Corpuz G.P., Cruz L.J.;  
Unpublished results, cited by:  
Olivera B.M., Rivier J.E., Clark C., Ramilo C.A., Corpuz G.P.,  
Abogadie F.C., Mena E.E., Woodward S.R., Hillyard D.R., Cruz L.J.;  
Science 249:257-263(1990).  
-!- SUBCELLULAR LOCATION: Secreted.  
-!- TISSUE SPECIFICITY: Expressed by the venom duct.  
-!- SIMILARITY: BELONGS TO THE M-SUPERFAMILY OF CONOTOXINS.  
KW Toxin; Hydroxylation.  
FT DISULFID 1 9 PROBABLE.  
FT DISULFID 2 12 PROBABLE.  
FT DISULFID 6 13 PROBABLE.  
FT MOD\_RES 11 11 HYDROXYLATION.  
SQ SEQUENCE 15 AA; 1724 MW; C9CEBA917BED832D CRC64;  
Query Match 21.1%; Score 26; DB 1; Length 15;  
Best Local Similarity 55.6%; Pred. No. 4.4e+02;  
Matches 5; Conservative 0; Mismatches 2; Indels 2; Gaps 1;  
3 WRCLIPAC 11  
|||||  
7 WVC--IPCC 13  
RESULT 20  
CXMA\_CONPE STANDARD; PRT; 17 AA.  
ID\_CXMA\_CONPE  
AC P38926;  
28-FEB-2003 (Rel. 41, Created)  
28-FEB-2003 (Rel. 41, Last sequence update)  
28-FEB-2003 (Rel. 41, Last annotation update)  
Mu-conotoxin PnIVA.  
DE DE  
OS Conus pennaceus (Feathered cone).  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;  
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;  
OC Neogastropoda; Conoidea; Conidae; Conus.  
NCBI\_TaxID=37335;  
[1]  
SEQUENCE. AND MASS SPECTROMETRY.  
MEDLINE=95337083; PubMed=7612605;  
Fainzilber M., Nakamura T., Gaathon A., Lodder J.C., Kits K.S.,  
Burlingame A.L., Zlotkin E.;  
"A new cysteine framework in sodium channel blocking conotoxins";  
Biochemistry 34:8649-8656(1995).  
-!- FUNCTION: Mu-conotoxins bind and block voltage-sensitive sodium  
channel. Blocks reversibly sodium currents in molluscan neurons, or  
but has no effect on sodium currents in bivalve mollusks  
in rat brain synaptosomes. Induces paralysis in bivalve mollusks  
(Mytilus). No effect are observed on fish (Gambusia) and fly  
larvae (Sarcophaga). PnIV is approximately 6 times more potent  
than PnIVA in blockade of the sodium current in Lymnaea neurons.  
-!- SUBCELLULAR LOCATION: Secreted.  
-!- TISSUE SPECIFICITY: Expressed by the venom duct.  
-!- MASS SPECTROMETRY: MW=1789.5; METHOD=LSIMS.  
-!- SIMILARITY: BELONGS TO THE M-SUPERFAMILY OF CONOTOXINS. MU-TYPE  
FAMILY.  
KW Toxin; Neurotoxin; Ionic channel inhibitor; Sodium channel inhibitor.  
FT SITE 4 4 IMPORTANT FOR BINDING AND ACTIVITY.  
FT DISULFID 1 12 BY SIMILARITY.  
FT DISULFID 2 15 BY SIMILARITY.

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1  DISULFID 8 17 BY SIMILARITY
2  SEQUENCE 17 AA; 1757 MW; F9B721E0F6B9D82 CRC64;
3
4  Query Match 20.3%; Score 25; DB 1; Length 17;
5  Best Local Similarity 42.9%; Pred. No. 6.9e+02;
6  Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
7
8  1 FNRWCCL 7
9  : |||
10 4 IGYTCLL 10
11
12 RESULT 21
13 1B CONBE STANDARD; PRT; 15 AA.
14 P58624;
15 28-FEB-2003 (Rel. 41, Created)
16 28-FEB-2003 (Rel. 41, Last sequence update)
17 28-FEB-2003 (Rel. 41, Last annotation update)
18 Conotoxin BetXib.
19 Conus betulinus (Beech cone).
20 Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
21 Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
22 Neogastropoda; Conoidea; Conidae; Conus.
23 NCBI_TaxID=89764;
24 [1]
25 SEQUENCE, AND MASS SPECTROMETRY.
26 TISSUE=Venom;
27 MEDLINE=20058566; PubMed=10591037;
28 Chen J.-S., Fan C.-X., Hu K.-P., Wei K.-H., Zhong M.-N.;
29 "Studies on conotoxins of Conus betulinus.";
30 J. Nat. Toxins 8:341-349(1999).
31 -1- SUBCELLULAR LOCATION: Secreted.
32 -1- TISSUE SPECIFICITY: Expressed by the venom duct.
33 -1- MASS SPECTROMETRY: MW=1642.5; METHOD=MALDI.
34 -1- SIMILARITY: BELONGS TO THE M-SUPERFAMILY OF CONOTOXINS.
35 Neurotoxin; Toxin.
36 DISULFID 1 9 PROBABLE.
37 DISULFID 2 12 PROBABLE.
38 DISULFID 6 13 PROBABLE.
39 SEQUENCE 15 AA; 1650 MW; 3749B4F08E311337 CRC64;
40
41 Query Match 19.5%; Score 24; DB 1; Length 15;
42 Best Local Similarity 60.0%; Pred. No. 8.6e+02;
43 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
44
45 5 CCLIP 9
46 : |||
47 1 CCELP 5
48
49 RESULT 22
50 X3A CONQU STANDARD; PRT; 15 AA.
51 P58841;
52 28-FEB-2003 (Rel. 41, Created)
53 28-FEB-2003 (Rel. 41, Last sequence update)
54 28-FEB-2003 (Rel. 41, Last annotation update)
55 Conotoxin OcIIIA.
56 Conus guercinus (Oak cone).
57 Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
58 Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
59 Neogastropoda; Conoidea; Conidae; Conus.
60 NCBI_TaxID=101313;
61 [1]
62 SEQUENCE.
63 MEDLINE=90327072; PubMed=2165278;
64 Abogadie F.C., Ramilo C.A., Corpuz G.P., Cruz L.J.;
65 Unpublished results, cited by:
66 Olivera B.M., Rivier J.E., Clark C., Ramilo C.A., Corpuz G.P.,
67 Abogadie F.C., Mena E.E., Woodward S.R., Hillyard D.R., Cruz L.J.;
68 Science 249:257-263(1990).
69 -1- FUNCTION: Causes scratching in mice.
70
71 CC -1- SUBCELLULAR LOCATION: Secreted.
72 CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
73 CC -1- SIMILARITY: BELONGS TO THE M-SUPERFAMILY OF CONOTOXINS.
74 KW Toxin; Hydroxylation; Amidation.
75 FT DISULFID 1 9 PROBABLE.
76 FT DISULFID 2 12 PROBABLE.
77 FT DISULFID 6 13 PROBABLE.
78 FT MOD_RES 11 11 HYDROXYLATION.
79 FT MOD_RES 15 15 AMIDATION.
80 SEQUENCE 15 AA; 1601 MW; D479B5AEB4ED832D CRC64;
81
82 Query Match 19.5%; Score 24; DB 1; Length 15;
83 Best Local Similarity 38.5%; Pred. No. 8.6e+02;
84 Matches 5; Conservative 0; Mismatches 2; Indels 6; Gaps 1;
85
86 QY 5 CC-----LIPAC 11
87 : |||
88 Db 1 CCSQDCLVCIPCC 13
89
90 RESULT 23
91 CXMB CONPE STANDARD; PRT; 17 AA.
92 AC P58927;
93 28-FEB-2003 (Rel. 41, Created)
94 28-FEB-2003 (Rel. 41, Last sequence update)
95 28-FEB-2003 (Rel. 41, Last annotation update)
96 Mu-conotoxin PnIVB.
97 Conus pennaceus (Feathered cone).
98 Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
99 Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
100 Neogastropoda; Conoidea; Conidae; Conus.
101 NCBI_TaxID=37335;
102 [1]
103 SEQUENCE, AND MASS SPECTROMETRY.
104 MEDLINE=95337083; PubMed=7612605;
105 Painsilber M., Nakamura T., Gaathon A., Lodder J.C., Kits K.S.,
106 Burlingame A.L., Zlotkin E.;
107 "A new cysteine framework in sodium channel blocking conotoxins.";
108 Biochemistry 34:8649-8656(1995).
109 [2]
110 PHARMACOLOGICAL CHARACTERIZATION.
111 MEDLINE=95346035; PubMed=7620628;
112 Haesson A., Painsilber M., Zlotkin E., Spira M.E.;
113 "Electrophysiological characterization of a novel conotoxin that
114 blocks molluscan sodium channels.";
115 Eur. J. Neurosci. 7:815-818(1995).
116 -1- FUNCTION: Mu-conotoxins bind and block voltage-sensitive sodium
117 channel. Blocks reversibly sodium channels in molluscan neurons,
118 but has no effect on sodium currents in bovine chromaffin cells or
119 in rat brain synaptosomes. Induces paralysis in bivalve mollusks
120 (Mytilus). No effect are observed on fish (Gambusia) and fly
121 larvae (Sarcophaga). Is approximately 6 times more potent than
122 PnIVA in blockade of the sodium current in Lymnaea neurons.
123 -1- SUBCELLULAR LOCATION: Secreted.
124 CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
125 CC -1- MASS SPECTROMETRY: MW=1862.8; METHOD=LSIMS.
126 CC -1- SIMILARITY: BELONGS TO THE M-SUPERFAMILY OF CONOTOXINS. MU-TYPE
127 FAMILY.
128 KW Toxin; Neurotoxin; Ionic channel inhibitor; Sodium channel inhibitor.
129 FT SITE 4 4 IMPORTANT FOR BINDING AND ACTIVITY (BY
130 SIMILARITY)
131 FT DISULFID 1 12 BY SIMILARITY.
132 FT DISULFID 2 15 BY SIMILARITY.
133 FT DISULFID 8 17 BY SIMILARITY.
134 SEQUENCE 17 AA; 1870 MW; E40021E0E96B9D82 CRC64;
135
136 Query Match 19.5%; Score 24; DB 1; Length 17;
137 Best Local Similarity 42.9%; Pred. No. 9.7e+02;
138 Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
139
140 QY 1 FNRWCCL 7
141 : |||

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4 YGWTCWL 10

ILT 24  
 \_ACTLG STANDARD; PRT; 19 AA.  
 P56650;  
 15-JUL-1999 (Rel. 38, Created)  
 28-FEB-2003 (Rel. 41, Last sequence update)  
 10-OCT-2003 (Rel. 42, Last annotation update)  
 Lanthibiotic actagardine (Gardimycin).  
 Actinoplanes liguriae.  
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 Micromonosporineae; Micromonosporaceae; Actinoplanes.  
 NCBI\_TaxID=69484;  
 [1]  
 PRELIMINARY SEQUENCE, AND STRUCTURE BY NMR.  
 MEDLINE=91008698; PubMed=2211371;  
 Kattenring J.K., Malabarba A., Vekey K., Cavallieri B.;  
 "Sequence determination of actagardine, a novel lantibiotic, by  
 homonuclear 2D NMR spectroscopy";  
 J. Antibiot. 43:1082-1088(1990).  
 [2]  
 SEQUENCE, AND STRUCTURE BY NMR.  
 MEDLINE=9525286; PubMed=7737178;  
 Zimmermann N., Metzger J.W., Jung G.;  
 "The tetracyclic lantibiotic actagardine. 1H-NMR and 13C-NMR  
 assignments and revised primary structure.";  
 Eur. J. Biochem. 228:786-797(1995).  
 [3]  
 STRUCTURE BY NMR.  
 MEDLINE=97363218; PubMed=9219543;  
 Zimmermann N., Jung G.;  
 "The three-dimensional solution structure of the lantibiotic murein-  
 biosynthesis-inhibitor actagardine determined by NMR.";  
 Eur. J. Biochem. 246:809-813(1997).  
 -1- FUNCTION: Has antibacterial activity against some Gram-positive  
 bacteria. Has good antistreptococcal activity.  
 -1- PTM: Maturation of lantibiotics involves the enzymic conversion of  
 Thr, and Ser into dehydrated AA and the formation of thioether  
 bonds with cysteines. The 14-19 beta-methylanthionine thioether  
 bond is oxidized to a sulfoxide. This is followed by membrane  
 translocation and cleavage of the modified precursor.  
 -1- SIMILARITY: Belongs to the type B lantibiotic family.  
 PIR; A58700; A58700.  
 PDB; 1A11; 15-OCT-97.  
 Antibiotic; Bacteriocin; Lantibiotic; Oxidation; Thioether bond;  
 3D-structure. 1 6 Lanthionine (Ser-Cys).  
 CROSSLINK 7 12 Beta-methylanthionine (Thr-Cys).  
 CROSSLINK 9 17 Beta-methylanthionine (Thr-Cys).  
 CROSSLINK 14 19 Beta-methylanthionine sulfoxide  
 (Thr-Cys).  
 SEQUENCE 19 AA; 1946 MW; 5C138C7CE8765B3 CRC64;

Query Match 19.5%; Score 24; DB 1; Length 19;  
 Best Local Similarity 44.4%; Pred. No. 1.1e+03;  
 Matches 4; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

ILT 25  
 P\_PETMA STANDARD; PRT; 19 AA.  
 Q10936;  
 01-OCT-1996 (Rel. 34, Created)  
 01-OCT-1996 (Rel. 34, Last sequence update)  
 15-MAR-2004 (Rel. 43, Last annotation update)  
 Corticostatin-related protein LCRP.  
 Petromyzon marinus (Sea lamprey).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;  
 OC Petromyzontiformes; Petromyzontidae; Petromyzon.  
 OX NCBI\_TaxID=7757;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Skin;  
 RX MEDLINE=96321324; PubMed=8759287;  
 RA Conlon J.M., Sower S.A.;  
 RT "Isolation of a peptide structurally related to mammalian  
 corticostatins from the lamprey Petromyzon marinus.";  
 RL Comp. Biochem. Physiol. 114B:133-137(1996).  
 CC -1- FUNCTION: May have microbicidal activities. May inhibit  
 corticotropin (ACTH) stimulated steroidogenesis and the microbial  
 actions of the corticostatins.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- MASS SPECTROMETRY: MW=2201; MW ERR=0.4; METHOD=Electrospray.  
 CC -1- SIMILARITY: Belongs to the corticostatin/defensin family.  
 KW Defensin; Antibiotic.  
 FT DISULFID 1 18 BY SIMILARITY.  
 FT DISULFID 3 9 BY SIMILARITY.  
 FT DISULFID 8 17 BY SIMILARITY.  
 SQ SEQUENCE 19 AA; 2209 MW; 8D9CEDC71A199AE5 CRC64;

Query Match 19.5%; Score 24; DB 1; Length 19;  
 Best Local Similarity 75.0%; Pred. No. 1.1e+03;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 4 RCCL 7  
 DB 7 RCCV 10

## RESULT 26

CONO\_CONST STANDARD; PRT; 9 AA.  
 AC P05487;  
 DT 01-NOV-1988 (Rel. 09, Created)  
 DT 01-NOV-1988 (Rel. 09, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Arg-conopressin S.  
 OS Conus striatus (Striated cone).  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;  
 OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;  
 OC Neogastropoda; Conoidea; Conidae; Conus.  
 OX NCBI\_TaxID=6493;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=89058932; PubMed=3680228;  
 RA Cruz L.J., de Santos V., Zafaralla G.C., Ramilo C.A., Zeikus R.D.,  
 Gray W.R., Olivera B.M., Cruz L.J.;  
 RA "Peptide toxins from venomous Conus snails.";  
 RT "Invertebrate vasopressin/oxytocin homologs. Characterization of  
 peptides from Conus geographus and Conus striatus venoms.";  
 RL J. Biol. Chem. 262:15821-15824(1987).  
 RN [2]  
 RP REVIEW.

Query Match 18.7%; Score 23; DB 1; Length 9;  
 Best Local Similarity 44.4%; Pred. No. 1.1e+03;  
 Matches 4; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

st Local Similarity 50.0%; Pred. No. 1.4e+05;  
tches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

6 CLIPACRR 13  
1 CLIRNCP 8

LT 27

CONVR  
CXL3 CONVR STANDARD; PRT; 12 AA.  
P58609;  
28-FEB-2003 (Rel. 41, Created)  
28-FEB-2003 (Rel. 41, Last sequence update)  
28-FEB-2003 (Rel. 41, Last annotation update)  
Lambda-conotoxin CMXX.  
Conus marmoreus (Marble cone).  
Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;  
Apogastropoda; Caenogastropoda; Sorbeconcha; Hypsogastropoda;  
Neogastropoda; Conoidea; Conidae; Conus.  
NCBI\_TaxID=42752;  
[1]

SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.

TISSUE=Venom;  
MEDLINE=20564325; PubMed=10988292;  
Balaji R.A., Ontake A., Sato K., Gopalakrishnakone P., Kini R.M.,  
Seow K.T., Bay B.-H.;  
"Lambda-conotoxins, a new family of conotoxins with unique disulfide  
pattern and protein folding. Isolation and characterization from the  
venom of Conus marmoreus.";  
J. Biol. Chem. 275:39516-39522(2000).  
-!- FUNCTION: Inhibits the neuronal noradrenaline transporter.  
-!- SUBCELLULAR LOCATION: Secreted.  
-!- TISSUE SPECIFICITY: Expressed by the venom duct.  
-!- MASS SPECTROMETRY: MW=1262.77; MW ERR=0.07; METHOD=Electrospray.  
-!- SIMILARITY: Belongs to the chi/lambda-conotoxin family.  
Neurotoxin; Toxin; Hydroxylation.  
DISULFID 3 12  
DISULFID 4 9  
MOD\_RES 11 11 HYDROXYLATION  
SEQUENCE 12 AA; 1251 MW; 277AAE2422D5AC8 CRC64;

ery Match 18.7%; Score 23; DB 1; Length 12;  
st Local Similarity 42.9%; Pred. No. 9.8e+02;  
tches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

5 CCLIPAC 11  
3 CCGVSFC 9

LT 28

ESTAC  
LYC ESTAC STANDARD; PRT; 18 AA.  
P82175;  
16-OCT-2001 (Rel. 40, Created)  
16-OCT-2001 (Rel. 40, Last sequence update)  
28-FEB-2003 (Rel. 41, Last annotation update)  
Lysozyme (EC 3.2.1.17) (1,4-beta-N-acetylmuramidase) (Fragment).  
Estigmenes acraea (Salt marsh moth).  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;  
Actiidae; Estigmenes.  
NCBI\_TaxID=56594;  
[1]

SEQUENCE, AND ENZYME REGULATION.

TISSUE=Hemocyte;  
MEDLINE=97448947; PubMed=9303271;  
Wittwer D., Weise C., Goetz P., Wiesner A.;  
"LPS (lipopolysaccharide)-activated immune responses in a hemocyte  
cell line from Estigmenes acraea (Lepidoptera).";  
Dev. Comp. Immunol. 21:323-336(1997).  
-!- FUNCTION: Lysozymes have primarily a bacteriolytic function; those

in tissues and body fluids are associated with the monocyte-  
macrophage system and enhance the activity of immunocagents (By  
similarity).

-!- CATALYTIC ACTIVITY: Hydrolysis of the 1,4-beta-linkages between N-  
acetyl-D-glucosamine and N-acetylmuramic acid in peptidoglycan  
heteropolymers of the prokaryotes cell walls.  
-!- ENZYME REGULATION: By lipopolysaccharide (LPS).  
-!- SIMILARITY: Belongs to family 22 of glycosyl hydrolases.  
DR InterPro: IPR001916; Glyco\_Hydro\_22.  
DR PROSITE: PS00128; LACTALBUMIN LYSOZYME; PARTIAL.  
KW Hydrolase; Glycosidase; Bacteriolytic enzyme.  
FT NON\_TER 18 18  
SQ SEQUENCE 18 AA; 2213 MW; B229D8F5ECD7F57 CRC64;

Query Match 18.7%; Score 23; DB 1; Length 18;  
Best Local Similarity 38.5%; Pred. No. 1.4e+03;  
Matches 5; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 FNRCCCLIPACRR 13  
DB 3 PATRCDDVRELK 15

RESULT 29

GON2\_CHEPR STANDARD; PRT; 10 AA.  
AC P80678;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Gonadoliberin II (Gonadotropin-releasing hormone II) (GnRH-II)  
DE (Luliberin II).  
OS Chelyosoma productum.  
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;  
OC Phlebobranchia; Corellidae; Chelyosoma.  
OX NCBI\_TaxID=71177;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=96413669; PubMed=8816823;  
RA Powell J.F.F., Reska-Skinner S.M., Prakash M.O., Fischer W.H.,  
RA Park M., Rivier J.E., Craig A.G., Mackie G.O., Sherwood N.M.;  
RT "Two new forms of gonadotropin-releasing hormone in a protochordate  
and the evolutionary implications.";  
RL Proc. Natl. Acad. Sci. U.S.A. 93:10461-10464(1996).  
CC -!- FUNCTION: Stimulates the secretion of gonadotropins; it stimulates  
the secretion of both luteinizing and follicle-stimulating  
hormones.  
CC -!- SUBUNIT: Homodimer; disulfide-linked.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: GnRH NEURONS LIE WITHIN BLOOD SINUSES CLOSE TO  
THE GONADUCTS AND GONADS IN BOTH JUVENILES AND ADULTS, IMPLYING  
THAT THE NEUROPEPTIDE IS RELEASED INTO THE BLOODSTREAM.  
CC -!- MASS SPECTROMETRY: MW=1117.52; METHOD=MALDI.  
CC -!- SIMILARITY: Belongs to the GnRH family.  
DR InterPro: IPR02012; GnRH.  
DR PROSITE: PS00473; GNRH.1.  
KW Hormone; Amidation; Pyrrolidone carboxylic acid.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT DISULFID 6 6 INTERCHAIN.  
FT MOD\_RES 10 10 AMIDATION (BY SIMILARITY).  
SQ SEQUENCE 10 AA; 1135 MW; 284B38D1EEB735A3 CRC64;

Query Match 17.9%; Score 22; DB 1; Length 10;  
Best Local Similarity 37.5%; Pred. No. 1.2e+03;  
Matches 3; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 NWRCCCLIP 9  
DB 2 HWSLCHAP 9

RESULT 30

TINI\_HOPTI

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TIN1 HOPTI STANDARD; PRT; 11 AA.
P82651;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Tigerin-1.
Hoplomatrachus tigrinus (Indian bull frog) (Rana tigerina).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae;
Hoplomatrachus.
NCBI_TaxID=103373;
[1]
SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND DISULFIDE BONDS.
TISSUE=Skin secretion;
PubMed11031261;
Purna Sai K., Nagaraj R., Sitaram N.;
"Vigilant: novel antimicrobial peptides from the Indian frog Rana
tigrina.";
J. Biol. Chem. 276:2701-2707(2001).
-!- FUNCTION: Antibacterial activity against B. subtilis, E. coli,
S. aureus, M. luteus, P. putida and S. cerevisiae.
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Skin.
-!- MASS SPECTROMETRY: MW=1342; METHOD=MALDI.
Amphibian defense peptide; Antibiotic; Fungicide; Amidation.
DISULFID 2 10
MOD RES 11 11
SEQUENCE 11 AA; 1344 MW; A2087DC960476056 CRC64;
Query Match 17.9%; Score 22; DB 1; Length 11;
St Local Similarity 50.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
5 CCLIPACR 12
: : : :
2 CTMIPR 9
[1]
LT 31
-CAVPO STANDARD; PRT; 15 AA.
P83508;
10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Major allergen Cav p 2 (Fragment).
Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
NCBI_TaxID=10141;
[1]
SEQUENCE
TISSUE=Hair;
MEDLINE=22707217; PubMed=12823123;
Fahlbusch B., Rudeschko O., Schlott B., Henzgen M., Schlenvoigt G.,
Schubert H., Kinne R.W.;
"Further characterization of IGS-binding antigens from guinea pig
hair as new members of the lipocalin family.";
Allergy 58:629-634(2003).
-!- SUBCELLULAR LOCATION: Secreted.
-!- ALLERGEN: Causes an allergic reaction in human. Binds to IgE. Is a
cause of guinea pig hair allergy.
-!- SIMILARITY: Belongs to the lipocalin family.
GO: GO:0016068; P: Immediate hypersensitivity response; NAS.
InterPro: IPR000566; Lipocalin, CYTAP.
PROSITE: PS00213; LIPOCALIN, PARTIAL.
Lipocalin; Allergen. 15
NON_TER 15
SEQUENCE 15 AA; 1751 MW; DGA0253A7A23EC26 CRC64;
Query Match 17.9%; Score 22; DB 1; Length 15;
St Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
TIN1 HOPTI STANDARD; PRT; 15 AA.
P80614;
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
DE Unknown protein from 2D-page of etiolated coleoptile (Spot 159)
(Fragment).
Zea mays (Maize).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
PACCAD clade; Panicoideae; Andropogoneae; Zea.
NCBI_TaxID=4577;
[1]
SEQUENCE.
RP TISSUE=Coleoptile;
Touzet P., Ricciardi F., Morin C., Damerval C., Huet J.-C.,
Pernollet J.-C., Ziwy M., de Vienne D.;
"The maize two dimensional gel protein database: towards an integrated
genome analysis program.";
Theor. Appl. Genet. 93:997-1005(1996).
CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
protein is: 6.4, its MW is: 38.8 kDa.
CC -!- SIMILARITY: Belongs to the zinc-containing alcohol dehydrogenase
family.
CC Maize-2DPAGE; P80614; COLEOPTILE.
DR MaizeDB; 123934; -.
FT NON_TER 1 1
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1785 MW; 1978B1D6AB4DDF8D CRC64;
Query Match 17.9%; Score 22; DB 1; Length 15;
Best Local Similarity 37.5%; Pred. No. 1.7e+03;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
OXYT BUFRE STANDARD; PRT; 9 AA.
AC P42955;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Seritocin [Sers, Iles]-oxytocin.
OS Bufo regularis (Leopard toad).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Bufonidae; Bufo.
NCBI_TaxID=8390;
[1]
SEQUENCE.
RP TISSUE=Hypothalamic neurointermediate lobe;
RC MEDLINE=96059313; PubMed=7591488;
RA Chauvet J., Michel G., Ouedraogo Y., Chou J., Chait B.T., Acher R.;
"A new neurohypophyseal peptide, seritocin [Sers, Iles]-oxytocin",
identified in a dryness-resistant African toad, Bufo regularis.";
Int. J. Pept. Protein Res. 45:482-487(1995).
RL Int. J. Pept. Protein Res. 45:482-487(1995).
CC -!- FUNCTION: Devoid of oxytocic activity.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the vasopressin/oxytocin family.
DR InterPro; IPR000981; Neurohyp_horm.
PFam; PF00220; hormone4; 1.
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PROSITE: PS00264; NEUROHYPOPHYS_HORM; FALSE_NEG.
Hormone; Amidation.
DISULFID 1 6
MOD_RES 9 9 AMIDATION.
SEQUENCE 9 AA; 983 MW; 17FF476EAS6D04B CRC64;
very Match 17.1%; Score 21; DB 1; Length 9;
est Local Similarity 50.0%; Pred. No. 1.4e+05;
atches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

6 CLIPAC 11
| | | |
1 CYIQSC 6

JLT 34
I_CYPCA STANDARD; PRT; 9 AA.
P23879;
01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
Vasotocin.
Cyprinus carpio (Common carp), and
Petrionyzon marinus (Sea lamprey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Cyprinus.
NCBI_TaxID=7962, 7757;
[1]
SEQUENCE.
SPECIES=C. carpio; TISSUE=Pituitary;
Acher R., Chauvet J., Chauvet M.-T., Crepy D.;
"Characterization of neurohypophyseal hormones from a fresh water bony
fish, the carp (Cyprinus carpio). Comparison with hormones from sea
water bony fishes.";
Comp. Biochem. Physiol. 14:245-254 (1965).
[2]
SEQUENCE.
SPECIES=P. marinus; TISSUE=Pituitary;
MEDLINE=88225976; PubMed=3371648;
Lane T.F., Sower S.A., Kawachi H.;
"Arginine vasotocin from the pituitary gland of the lamprey
(Petrionyzon marinus): isolation and amino acid sequence.";
Gen. Comp. Endocrinol. 70:152-157 (1988).
-!- FUNCTION: ANTIDIURETIC HORMONE.
-!- SIMILARITY: Belongs to the vasopressin/oxytocin family.
PIR: B61364; B61364.
PIR: S06375; S06375.
InterPro: IPR000981; Neurohyp_horm.
Pfam: PF00220; hormones4; 1.
PROSITE: PS00264; NEUROHYPOPHYS_HORM; 1.
Hormone; Amidation.
DISULFID 1 6
MOD_RES 9 9 AMIDATION.
SEQUENCE 9 AA; 1053 MW; 17EB176EB456D04B CRC64;
very Match 17.1%; Score 21; DB 1; Length 9;
est Local Similarity 50.0%; Pred. No. 1.4e+05;
atches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

6 CLIPACR 13
| | | |
1 CYIQNCP 8

JLT 35
A_CATCO STANDARD; PRT; 12 AA.
P04558;
13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)

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```

DE Urotensin IIA (U-IIA) (UIIA).
OS Catostomus commersoni (White sucker).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Catostomidae; Catostomus.
OX NCBI_TaxID=7971;
RN [1]
RP SEQUENCE.
RX MEDLINE=84041959; PubMed=6138758;
RA McMaster D., Lederis K.;
RT "Isolation and amino acid sequence of two urotensin II peptides from
RT Catostomus commersoni urophyses.";
RL Peptides 4:367-373 (1983).
CC -!- FUNCTION: Urotensin is found in the teleost caudal neurosecretory
CC system. It has a suggested role in osmoregulation and as a
CC corticotropin-releasing factor.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the urotensin 2 family.
DR FIR; JS0423; JS0423.
DR InterPro: IPR001483; Urotensin_II.
DR Pfam: PF02083; Urotensin_II; 1.
DR PROSITE: PS00984; UROTENSIN_II; 1.
KW Hormone.
FT DISULFID 6 11
SQ SEQUENCE 12 AA; 1336 MW; 969C76DBB879CEBA CRC64;
Query Match 17.1%; Score 21; DB 1; Length 12;
Best Local Similarity 40.0%; Pred. No. 1.9e+03;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 WRCCCL 7
| | | |
Db 8 WKYCV 12

Search completed: February 18, 2004, 06:27:56
Job time : 13 secs

```

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

protein - protein search, using sw model

on: February 18, 2004, 06:15:19 ; Search time 38 seconds  
(without alignments)  
157.759 Million cell updates/sec

le: US-09-806-376-1

fect score: 123

lence: 1 FNRWCLIPACRNHHKFC 19

ring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

ched: 1017041 seqs, 315518202 residues

al number of hits satisfying chosen parameters: 6498

imum DB seq length: 0

imum DB seq length: 19

t-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

abase : SPTREMBL 25:\*

1: sp\_archaea:\*

2: sp\_bacteria:\*

3: sp\_fungi:\*

4: sp\_human:\*

5: sp\_invertebrate:\*

6: sp\_mammal:\*

7: sp\_mhc:\*

8: sp\_organelle:\*

9: sp\_phage:\*

10: sp\_plant:\*

11: sp\_rodent:\*

12: sp\_virus:\*

13: sp\_vertebrate:\*

14: sp\_unclassified:\*

15: sp\_virus:\*

16: sp\_bacteriap:\*

17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

ult No.	Score	Query Match	Length	ID	Description
1	36	29.3	9	10 Q9FSZ2	Q9fsz2 cicer ariet
2	30	24.4	19	12 Q65340	Q65340 autographa
3	29	23.6	13	4 QJUM29	QJum29 homo sapien
4	29	23.6	17	4 Q16228	Q16228 homo sapien
5	28.5	23.2	17	6 QXSG1	QXsg1 bos taurus
6	28	22.8	10	8 Q9T2P3	Q9t2p3 rattus sp.
7	28	22.8	17	5 Q9T6R4	Q9t6r4 conus imper
8	27.5	22.4	17	2 Q9R581	Q9r581 vibrio chol
9	27.5	22.4	18	2 Q9R580	Q9r580 vibrio chol
10	27.5	22.4	19	2 Q9R579	Q9r579 vibrio chol
11	27	22.0	15	4 Q15344	Q15344 homo sapien
12	26	21.1	15	15 Q85713	Q85713 rous sarcom
13	26	21.1	19	11 Q8CJ05	Q8cj05 mesocricetu
14	25	20.3	14	4 Q9BX07	Q9bx07 homo sapien
15	25	20.3	15	2 Q7WR21	Q7wr21 flavobacter
16	25	20.3	17	5 Q816R5	Q816r5 conus imper

17	25	20.3	19	15	Q905K4	Q905k4 human immun
18	24	19.5	8	11	Q80WD6	Q80wd6 mus musculus
19	24	19.5	8	11	Q80WD5	Q80wd5 mus musculus
20	24	19.5	11	11	Q87330	Q87330 mus musculus
21	24	19.5	11	12	Q89269	Q89269 xestia c-ni
22	24	19.5	11	13	Q9P222	Q9p222 xenopus lae
23	24	19.5	17	4	Q86V63	Q86v63 homo sapien
24	24	19.5	17	12	Q8B4C4	Q8b4c4 hepatitis b
25	24	19.5	18	8	Q78379	Q78379 theileria a
26	24	19.5	19	4	Q9UMM9	Q9umm9 homo sapien
27	24	19.5	19	8	Q9XMB5	Q9xmb5 aegilops ta
28	23	18.7	12	12	Q88577	Q88577 theiler's e
29	23	18.7	12	12	Q88578	Q88578 theiler's e
30	23	18.7	12	12	Q88579	Q88579 theiler's e
31	23	18.7	12	12	Q88575	Q88575 theiler's e
32	23	18.7	12	12	Q88580	Q88580 theiler's e
33	23	18.7	12	12	Q88582	Q88582 theiler's e
34	23	18.7	12	12	Q88581	Q88581 theiler's e
35	23	18.7	12	12	Q88576	Q88576 theiler's e
36	23	18.7	13	12	Q9ELV1	Q9elv1 hepatitis b
37	23	18.7	19	8	Q9ZIW7	Q9ziw7 aphidius ro
38	23	18.7	19	8	Q9ZYW5	Q9zyw5 jarra phoro
39	23	18.7	19	8	Q9ZY71	Q9zy71 heterospilu
40	23	18.7	19	11	Q925G8	Q925g8 mus musculus
41	23	18.7	19	15	Q90RG1	Q90rg1 human immun
42	22	17.9	8	6	Q02831	Q02831 oryctolagus
43	22	17.9	13	8	Q9T569	Q9t569 zea mays (m
44	22	17.9	13	11	Q60517	Q60517 mus musculus
45	22	17.9	14	2	P71199	P71199 escherichia
46	22	17.9	14	2	Q93C11	Q93c11 escherichia
47	22	17.9	14	11	Q81027	Q81027 mus musculus
48	22	17.9	16	12	Q9YQ11	Q9yq11 transmissib
49	22	17.9	16	13	Q9PTT5	Q9ptt5 gallus gall
50	22	17.9	17	2	Q841R6	Q841r6 yersinia pe

## ALIGNMENTS

### RESULT 1

Q9FSZ2	PRELIMINARY;	PRT;	9 AA.
ID	Q9FSZ2		
AC	Q9FSZ2;		
DT	01-MAR-2001 (TrEMBLrel. 16, Created)		
DT	01-MAR-2001 (TrEMBLrel. 16, Last sequence update)		
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)		
DE	Hypothetical protein (Fragment).		
OS	Cicer arietinum (Chickpea) (Garbanzo)		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;		
OC	eurosid1; Fabales; Fabaceae; Papilionoideae; Cicereae; Cicer.		
OX	NCBI_TaxID=3827;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=cv. Castellana; TISSUE=Etolated epicotyl;		
RA	Dopico B.; Jimenez T.; Labrador E.;		
RT	"cDNA clones expressed in etolated Cicer arietinum epicotyls."		
RL	Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AJ299069; CAC10216.1; -		
KW	Hypothetical protein.		
FT	NON TER		
SQ	SEQUENCE 9 AA; 990 MW; 94413DDAA7272EBE CRC64;		

Query Match 29.3%; Score 36; DB 10; Length 9;  
Best Local Similarity 71.4%; Pred. NO. 1e+06;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY	5 CCLIPAC 11
DB	2 CCLDAD 8

### RESULT 2



340 Q65340 PRELIMINARY; PRT; 19 AA.  
Q65340;  
01-NOV-1996 (TReMBLrel. 01, Created)  
01-NOV-1996 (TReMBLrel. 01, Last sequence update)  
01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
DNA polymerase (Fragment).  
Autographa californica nuclear polyhedrosis virus (AcNPV).  
Viruses; dsDNA viruses, no RNA stage; Baculoviridae;  
Nucleopolyhedrovirus.  
NCBI\_TaxID=46015;  
[1]  
SEQUENCE FROM N.A.  
STRAIN=L1;  
MEDLINE=89073763; PubMed=3059678;  
Tonalski M.D., Wu J., Miller L.K.;  
"The location, sequence, transcription, and regulation of a  
baculovirus DNA polymerase gene.";  
Virology 167:591-600(1988).  
[2]  
SEQUENCE FROM N.A.  
STRAIN=L1;  
MEDLINE=89381697; PubMed=2674327;  
Wu J., Miller L.K.;  
"Sequence, transcription and translation of a late gene of the  
Autographa californica nuclear polyhedrosis virus encoding a 34.8K  
polypeptide.";  
J. Gen. Virol. 70:2449-2459(1989).  
EMBL; D00583; BAA00460.1; --  
NON TER 1  
SEQUENCE 19 AA; 2314 MW; C9DD06D721F17972 CRC64;

Query Match 24.4%; Score 30; DB 12; Length 19;  
Best Local Similarity 55.6%; Pred. No. 7.1e+02;  
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
atches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
11 CRRNHKFC 19  
| | | | |  
5 CANTYKFC 13

ULT 3  
MB9  
Q9UME9 PRELIMINARY; PRT; 13 AA.  
Q9UME9;  
01-MAY-2000 (TReMBLrel. 13, Created)  
01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
01-MAY-2000 (TReMBLrel. 13, Last annotation update)  
Elastin (Fragment).  
ELN.  
Homo sapiens (Human).  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
NCBI\_TaxID=9606;  
[1]  
SEQUENCE FROM N.A.  
MEDLINE=87274906; PubMed=3038460;  
Indik Z., Yoon K., Morrow S.D., Cicila G., Rosenbloom J.,  
Rosenbloom J., Ornstein-Goldstein N.;  
"Structure of the 3' region of the human elastin gene: great abundance  
of Alu repetitive sequences and few coding sequences.";  
Connect. Tissue Res. 16:197-211(1987).  
[2]  
SEQUENCE FROM N.A.  
MEDLINE=93091639; PubMed=9873040;  
Zhang M.C., He L., Giro M., Yong S.L., Tiller G.E., Davidson J.M.;  
"Curis laxa arising from frameshift mutations in exon 30 of the  
elastin gene (ELN).";  
J. Biol. Chem. 274:981-986(1999).  
EMBL; U77846; AAC99789.1; --  
NON TER 1  
SEQUENCE 13 AA; 1348 MW; 43E12DFB5AE5BDD3 CRC64;

Query Match 23.6%; Score 29; DB 4; Length 13;  
Best Local Similarity 54.5%; Pred. No. 7.3e+02;  
Matches 6; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
QY 6 CLIPACRRNHK 16  
| | | | |  
DB 3 CLGKACGRK 13  
| | | | |  
RESULT 4  
Q16228 PRELIMINARY; PRT; 17 AA.  
ID Q16228;  
AC Q16228;  
DT 01-NOV-1996 (TReMBLrel. 01, Created)  
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)  
DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)  
DE Peripherin (Fragment).  
GN RDS.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=94290510; PubMed=8019570;  
RA Gruning G., Millan J.M., Meins M., Beneyto M., Caballero M.,  
Apfelstedt-Sylla E., Bosch R., Zrenner E., Prieto F., Gal A.;  
RT "Mutations in the human peripherin/RDS gene associated with autosomal  
dominant retinitis pigmentosa.";  
Hum. Mutat. 3:321-323(1994).  
RL EMBL; S73627; AAB31191.1; --  
FT NON TER 1  
SQ SEQUENCE 17 AA; 2342 MW; 96828BA695A9D1EB CRC64;

Query Match 23.6%; Score 29; DB 4; Length 17;  
Best Local Similarity 38.9%; Pred. No. 9.3e+02;  
Matches 7; Conservative 2; Mismatches 5; Indels 4; Gaps 1;  
QY 1 FNRWCLIPACRRNHKFF 18  
| | | | |  
DB 1 WRWR----RACRRPGRPF 14

RESULT 5  
Q9XSG1 PRELIMINARY; PRT; 17 AA.  
ID Q9XSG1  
AC Q9XSG1;  
DT 01-NOV-1999 (TReMBLrel. 12, Created)  
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)  
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)  
DE SMCX (Fragment).  
GN SMCX.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RA Poloumienko A., Blecher S.;  
RT "Exon-intron structure of SMCX and SMCY genes in bovine and swine.";  
Submitted (MAR-1999) to the EMBL/GenBank/DDJ databases.  
RL EMBL; AF135448; AAD34440.1; --  
FT NON TER 1  
FT NON TER 17  
SQ SEQUENCE 17 AA; 1927 MW; 10351B0D516D16F0 CRC64;

Query Match 23.2%; Score 28.5; DB 6; Length 17;  
Best Local Similarity 55.8%; Pred. No. 1.1e+03;  
Matches 5; Conservative 0; Mismatches 1; Indels 3; Gaps 1;  
QY 3 WRCLIPAC 11

|||||  
9 WRC---PKC 14  
PRT; 10 AA.  
Q9T2P3 PRELIMINARY;  
Q9T2P3; PRT; 10 AA.  
01-MAY-2000 (TrEMBLrel. 13, Created)  
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
Cytochrome P-450 27/25-HYDROXYLASE=52 kDa isoform (Fragment).  
Rattus sp.  
Mitochondrion.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
NCBI\_TaxID=10118;  
[1]  
SEQUENCE.  
MEDLINE=91355184; PubMed=1893820;  
Addya S., Zheng Y.M., Shayig R.M., Fan J.Y., Avadhani N.G.;  
"Characterization of a female-specific hepatic mitochondrial  
cytochrome P-450 whose steady-state level is modulated by  
testosterone.";  
Biochemistry 30:8323-8330(1991).  
NON\_TER 1  
NON\_TER 10  
SEQUENCE 10 AA; 1092 MW; 316CFEFA072DDC7 CRC64;

Query Match 22.8%; Score 28; DB 8; Length 10;  
Best Local Similarity 55.8%; Pred. No. 8.5e+02;  
Matches 5; Conservative 2; Mismatches 0; Gaps 0;

8 IPACRRNHK 16  
|||||  
2 IPALRDHE 10

ULT 7  
Q816R4 PRELIMINARY; PRT; 17 AA.  
Q816R4;  
01-MAR-2003 (TrEMBLrel. 23, Created)  
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
Alpha-conotoxin ImI precursor (Fragment).  
Conus imperialis (Imperial cone).  
Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;  
Apogastropoda; Caenogastropoda; Sotbeoconcha; Hypsogastropoda;  
Neogastropoda; Conoidea; Conidae; Conus.  
NCBI\_TaxID=35631;  
[1]  
SEQUENCE FROM N.A.  
PubMed=12384509;  
Ellison M.A., McIntosh J.M., Olivera B.M.;  
"alpha-Conotoxins ImI and ImII: similar alpha 7 nicotinic receptor  
antagonists act at different sites.";  
J. Biol. Chem. 278:757-764(2003).  
EMBL; AY159318; AAN78128.1; -  
NON\_TER 1  
NON\_TER 5  
CHAIN 17 AA; 1938 MW; 9590D9CEA50279CF CRC64;  
SEQUENCE 17 AA; 1938 MW; 9590D9CEA50279CF CRC64;

Query Match 22.8%; Score 28; DB 5; Length 17;  
Best Local Similarity 57.1%; Pred. No. 1.3e+03;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

5 CCLIPAC 11  
|||||  
6 CCSDPRC 12

ULT 8

Q9R581  
ID Q9R581 PRELIMINARY; PRT; 17 AA.  
AC Q9R581;  
01-MAY-2000 (TrEMBLrel. 13, Created)  
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE 01-ST-1, NAG-ST, VM-ST-HEAT-stable enterotoxin.  
OS Vibrio cholerae.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;  
OC Vibrionaceae; Vibrio.  
OX NCBI\_TaxID=666;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=93314823; PubMed=8325391;  
Yoshino K., Miyachi M., Takao T., Bag P.K., Huang X., Nair G.B.,  
Takeda T., Shimonishi Y.;  
"Purification and sequence determination of heat-stable enterotoxin  
elaborated by a cholera toxin-producing strain of Vibrio cholerae  
O1.";  
FEBS Lett. 326:83-86(1993).  
RL HSP; P01559; 1ETN.  
DR GO:0005576; C:extracellular; IEA.  
DR GO:0015070; P:toxin activity; IEA.  
DR GO:0009405; P:pathogenesis; IEA.  
DR InterPro: IPR001489; Enterotoxin\_HS.  
DR Pfam: PF02048; Enterotoxin\_HS; 1.  
DR PROSITE; PS00273; ENTEROTOXIN\_H\_STABLE; 1.  
SQ SEQUENCE 17 AA; 1821 MW; 30FF036D018D601C CRC64;

Query Match 22.4%; Score 27.5; DB 2; Length 17;  
Best Local Similarity 60.0%; Pred. No. 1.6e+03;  
Matches 6; Conservative 0; Mismatches 1; Indels 3; Gaps 1;

QY 5 CCLI---PAC 11  
|||||  
DB 3 CCEICNPAC 12

RESULT 9  
Q9R580  
ID Q9R580 PRELIMINARY; PRT; 18 AA.  
AC Q9R580;  
01-MAY-2000 (TrEMBLrel. 13, Created)  
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE 01-ST-2, VC-H-ST-HEAT-stable enterotoxin.  
OS Vibrio cholerae.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;  
OC Vibrionaceae; Vibrio.  
OX NCBI\_TaxID=666;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=93314823; PubMed=8325391;  
Yoshino K., Miyachi M., Takao T., Bag P.K., Huang X., Nair G.B.,  
Takeda T., Shimonishi Y.;  
"Purification and sequence determination of heat-stable enterotoxin  
elaborated by a cholera toxin-producing strain of Vibrio cholerae  
O1.";  
FEBS Lett. 326:83-86(1993).  
RL HSP; P01559; 1ETN.  
DR GO:0005576; C:extracellular; IEA.  
DR GO:0015070; P:toxin activity; IEA.  
DR GO:0009405; P:pathogenesis; IEA.  
DR InterPro: IPR001489; Enterotoxin\_HS.  
DR Pfam: PF02048; Enterotoxin\_HS; 1.  
DR PROSITE; PS00273; ENTEROTOXIN\_H\_STABLE; 1.  
SQ SEQUENCE 18 AA; 1934 MW; 3080692D018D601C CRC64;

Query Match 22.4%; Score 27.5; DB 2; Length 18;  
Best Local Similarity 60.0%; Pred. No. 1.7e+03;  
Matches 6; Conservative 0; Mismatches 1; Indels 3; Gaps 1;

QY 5 CCLI---PAC 11

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||| |||
4 CCEICCPAC 13

ULT 10
579
Q9R579 PRELIMINARY; PRT; 19 AA.
Q9R579;
01-MAY-2000 (TReMBLrel. 13, Created)
01-MAY-2000 (TReMBLrel. 13, Last sequence update)
01-JUN-2003 (TReMBLrel. 24, Last annotation update)
01-ST-3=HEAT-stable enterotoxin.
Vibrio cholerae.
Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Vibrio.
NCBI_TaxID=666;
[1]
SEQUENCE
MEDLINE=93314823; PubMed=8325391;
Yoshino K., Miyachi M., Takao T., Bag P.K., Huang X., Nair G.B.,
Takeda T., Shimonishi Y.;
"Purification and sequence determination of heat-stable enterotoxin
elaborated by a cholera toxin-producing strain of Vibrio cholerae
O1";
FEBS Lett. 326:83-86(1993).
HSGP; P01559; IETN.
GO; GO:0005576; C:extracellular; IEA.
GO; GO:0015070; F:toxin activity; IEA.
GO; GO:0009405; P:pathogenesis; IEA.
InterPro: IPR001489; Enterotoxin HS.
Pfam: PF02048; Enterotoxin HS; 1.
PROSITE: PS00273; ENTEROTOXIN_H STABLE; 1.
SEQUENCE 19 AA; 2048 MW; 308015F1A18D601C CRC64;

Query Match 22.4%; Score 27.5; DB 2; Length 19;
Best Local Similarity 60.0%; Pred. No. 1.8e+03;
Matches 6; Conservative 0; Mismatches 1; Indels 3; Gaps 1;

5 CCLI---PAC 11
||| |||
5 CCEICCPAC 14

ULT 11
344
Q15344 PRELIMINARY; PRT; 15 AA.
Q15344;
01-NOV-1996 (TReMBLrel. 01, Created)
01-NOV-1999 (TReMBLrel. 12, Last sequence update)
01-NOV-1999 (TReMBLrel. 12, Last annotation update)
Aml1 protein (Fragment).
AML1.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
MEDLINE=96226397; PubMed=8631417;
Levanon D., Bernstein Y., Negreanu V., Ghazi M.C., Bar-Am I.,
Aloya R., Goldenberg D., Lotem J., Groner Y.;
"A large variety of alternatively spliced and differentially expressed
mRNAs are encoded by the human acute myeloid leukemia gene AML1.";
DNA Cell Biol. 15:175-185(1996).
EMBL; X90980; CAA62467.2; -.
NON_TER 1
NON_TER 15
NON_TER 15
SEQUENCE 15 AA; 1931 MW; 228A48BEE675423 CRC64;

Query Match 22.0%; Score 27; DB 4; Length 15;
Best Local Similarity 80.0%; Pred. No. 1.7e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 9 PACRR 13
|:|:|
Db 9 PSRR 13

RESULT 12
Q85713 PRELIMINARY; PRT; 15 AA.
Q85713;
AC Q85713;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE 29 (RSV-29) src (Fragment).
OS Rous sarcoma virus.
OC Viruses; Retroviral viruses; Retroviridae; Alpharetrovirus.
OX NCBI_TaxID=11886;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85265036; PubMed=2991593;
Dutta A., Wang L.-H., Hanafusa T., Hanafusa H.;
"Partial nucleotide sequence of Rous sarcoma virus-29 provides
RT evidence that the original rous sarcoma virus was replication
RT defective.";
RL J. Virol. 55:728-735(1985).
DR EMBL; M1117; AAA42556.1; -.
FT NON_TER 1
SQ SEQUENCE 15 AA; 1597 MW; DB5350F31273C5C1 CRC64;

Query Match 21.1%; Score 26; DB 15; Length 15;
Best Local Similarity 80.0%; Pred. No. 2.5e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 LIPAC 11
|:|:|
Db 5 LLPAC 9

RESULT 13
Q8CJ05 PRELIMINARY; PRT; 19 AA.
Q8CJ05;
AC Q8CJ05;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Cyclin D1 (Fragment).
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_TaxID=10036;
[1]
RP SEQUENCE FROM N.A.
RA Hilton T.L., Dunphy E.L., Wang E.H.;
"TAFL1 (TAFL1250), Histone Acetyltransferase Activity in Activation of
RT the Cyclin D1 Proximal Promoter.";
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF539477; AAN59789.1; -.
FT NON_TER 19
FT NON_TER 19
SQ SEQUENCE 19 AA; 2307 MW; 83E3341F29C52279 CRC64;

Query Match 21.1%; Score 26; DB 11; Length 19;
Best Local Similarity 44.4%; Pred. No. 3.1e+03;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 5 CCLIPACRR 13
|:|:|
Db 7 CCEVETIRR 15

RESULT 14
Q9BXR7 PRELIMINARY; PRT; 14 AA.
Q9BXR7;
ID Q9BXR7
AC Q9BXR7;
```

01-JUN-2001 (TrEMBLrel. 17, Created)  
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
Interleukin 10 (Fragment)  
Homo sapiens (Human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
NCBI\_TaxID=9606;  
[1]  
SEQUENCE FROM N.A.  
MEDLINE=21136366; PubMed=11238636;  
Gibson A.W., Edberg J.C., Wu J., Westendorp R.G.J., Huizinga T.W.J.,  
Kimberly R.P.;  
"Novel Single Nucleotide Polymorphisms in the Distal IL-10 Promoter  
Affect IL-10 Production and Enhance the Risk of Systemic Lupus  
Erythematosus.";  
J. Immunol. 166:3915-3922 (2001).  
EMBL; AF295024; AAK19173.1; -  
NON TER 14  
SEQUENCE 14 AA; 1504 MW; 438B64AB431997B7 CRC64;

Query Match 20.3%; Score 25; DB 4; Length 14;  
Best Local Similarity 75.0%; Pred. No. 3.4e+03;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

5 CCLJ 8  
|||:  
8 CCLV 11

JUL 15  
RZ1  
QWRZ1 PRELIMINARY; PRT; 15 AA.  
01-OCT-2003 (TrEMBLrel. 25, Created)  
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
Hypothetical protein.  
Bacteria; Bacteroidetes; Flavobacteriia; Flavobacteriales;  
Flavobacteriaceae; Flavobacterium.  
NCBI\_TaxID=96345;  
[1]  
SEQUENCE FROM N.A.  
STRAIN=FFC817, Ch. 8-80, TG-P01/88, OKW9801, OKW9801, YMY9520, YNU9803,  
FPC945, FPC940, FPC924, FPC956, OKA9805, and YNA9801;  
Izumi S., Aranishi F., Wakabayashi H.;  
"Genotyping of Flavobacterium psychrophilum using PCR-RFLP analysis.";  
Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.  
EMBL; AB097201; BAC76960.1; -  
EMBL; AB097202; BAC76961.1; -  
EMBL; AB097203; BAC76962.1; -  
EMBL; AB097204; BAC76963.1; -  
EMBL; AB097205; BAC76964.1; -  
EMBL; AB097206; BAC76965.1; -  
EMBL; AB097207; BAC76966.1; -  
EMBL; AB097208; BAC76967.1; -  
EMBL; AB097209; BAC76968.1; -  
EMBL; AB097210; BAC76969.1; -  
EMBL; AB097211; BAC76970.1; -  
EMBL; AB097212; BAC76971.1; -  
EMBL; AB097213; BAC76972.1; -  
Hypothetical protein.  
SEQUENCE 15 AA; 1903 MW; 668EE50085B3F71D CRC64;

Query Match 20.3%; Score 25; DB 2; Length 15;  
Best Local Similarity 42.9%; Pred. No. 3.6e+03;  
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

12 RNNKXF 18  
:|:|:  
9 KKNHAKY 15

RESULT 16  
Q816RS PRELIMINARY; PRT; 17 AA.  
AC Q816RS;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Alpha-conotoxin ImI precursor (Fragment).  
OS Conus imperialis (Imperial cone).  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;  
OC Apogastropoda; Caenogastropoda; Sorbecconcha; Hypogastropoda;  
OC Neogastropoda; Conoidea; Conidae; Conus.  
OX NCBI\_TaxID=35631;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX PubMed=12384509;  
RA Ellison M.A., McIntosh J.M., Olivera B.M.;  
RT "alpha-Conotoxins ImI and ImII: similar alpha 7 nicotinic receptor  
antagonists act at different sites.";  
RL J. Biol. Chem. 278:757-764 (2003).  
DR EMBL; AY159317; AAN78127.1; -  
FT NON TER 1  
FT CHAIN 5 17 ALPHA-CONOTOXIN IMI.  
SQ SEQUENCE 17 AA; 2096 MW; CF90D9CEBB4C79CC CRC64;

Query Match 20.3%; Score 25; DB 5; Length 17;  
Best Local Similarity 100.0%; Pred. No. 4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 WRC 5  
|||:  
Db 14 WRC 16

RESULT 17  
Q905K4 PRELIMINARY; PRT; 19 AA.  
AC Q905K4;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE Tat protein (Fragment).  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=96CG16;  
RA Taniguchi Y., Takehsia J., Bikandou B., Mboudjeka I.,  
RA N'Doundou-N'Kodia M.-Y., M'Pandi M., M'Pepe P., Harada Y., Hayami M.,  
RA Ichimura H., Parra H.-J.;  
RT "Genetic Subtypes of HIV Type 1 Based on the vpu/env Sequences in  
RT Republic of Congo-Brazzaville.";  
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF410438; AAL10218.1; -  
FT NON TER 1  
FT NON TER 19  
FT NON TER 19  
SQ SEQUENCE 19 AA; 2224 MW; B479FE3CB9E68238 CRC64;

Query Match 20.3%; Score 25; DB 15; Length 19;  
Best Local Similarity 40.0%; Pred. No. 4.4e+03;  
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 9 PACRRNHKXF 18  
:|:|:  
Db 7 PNSNQHQDF 16

RESULT 18  
Q80WD6 PRELIMINARY; PRT; 8 AA.  
ID Q80WD6  
AC Q80WD6;

01-JUN-2003 (TReMBLrel. 24, Created)  
 01-JUN-2003 (TReMBLrel. 24, Last sequence update)  
 01-OCT-2003 (TReMBLrel. 25, Last annotation update)  
 Olfactory receptor (Fragment).  
 GENE 154  
 Mus musculus (Mouse).  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCB1\_TaxID=10090;  
 [1]  
 SEQUENCE FROM N.A.  
 MEDLINE=94373818; PubMed=8087849;  
 Chessa A., Simon I., Cedar H., Axel R.;  
 "Allelic inactivation regulates olfactory receptor gene expression.";  
 Cell 78:823-834(1994).  
 EMBL; S73844; AAP21082.1; -.  
 GO; GO:0004872; F:receptor activity; IEA.  
 Receptor.  
 NON TER  
 SEQUENCE 8 AA; 1000 MW; F161A1E454140B16 CRC64;  
 Query Match 19.5%; Score 24; DB 11; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 [1]  
 12 RRNH 15  
 |||||  
 3 RRNH 6  
 RESULT 19  
 ID P89269 PRELIMINARY; PRT; 8 AA.  
 AC P89269;  
 DT 01-JUN-2003 (TReMBLrel. 24, Created)  
 DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)  
 DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)  
 Olfactory receptor (Fragment).  
 GENE 154.  
 Mus spretus (Western wild mouse).  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCB1\_TaxID=10096;  
 [1]  
 SEQUENCE FROM N.A.  
 MEDLINE=94373818; PubMed=8087849;  
 Chessa A., Simon I., Cedar H., Axel R.;  
 "Allelic inactivation regulates olfactory receptor gene expression.";  
 Cell 78:823-834(1994).  
 EMBL; S73845; AAP21082.1; -.  
 GO; GO:0004872; F:receptor activity; IEA.  
 Receptor.  
 NON TER  
 SEQUENCE 8 AA; 986 MW; F165B1E454140B16 CRC64;  
 Query Match 19.5%; Score 24; DB 11; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 [1]  
 12 RRNH 15  
 |||||  
 3 RRNH 6  
 RESULT 20  
 ID P97330 PRELIMINARY; PRT; 11 AA.  
 AC P97330;  
 DT 01-MAY-1997 (TReMBLrel. 03, Created)  
 DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)  
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
 CD45-AP (LSM-1).  
 PTPRCAP.

OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCB1\_TaxID=10090;  
 RW [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97124850; PubMed=8954783;  
 RA Bruyns E., Mincheva A., Bruyns R.M., Kirchgessner H., Weitz S.,  
 RA Lichter P., Meyer S., Schraven B.;  
 RT "Sequence, genomic organization and chromosomal localization of the  
 RT human LPAp (PTPRCAP) and Mouse CD45-AP/LSM-1 genes.";  
 RL Genomics 38:79-83(1996).  
 DR EMBL; X97268; CAA65923.1; -.  
 DR MGI; MGI:97811; Ptprcap.  
 SQ SEQUENCE 11 AA; 1150 MW; 50695413B5A772C7 CRC64;  
 Query Match 19.5%; Score 24; DB 11; Length 11;  
 Best Local Similarity 60.0%; Pred. No. 4e+03;  
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 CLIPA 10  
 |||||  
 DB 3 CLVPS 7  
 RESULT 21  
 ID P89269 PRELIMINARY; PRT; 11 AA.  
 AC P89269;  
 DT 01-MAY-1997 (TReMBLrel. 03, Created)  
 DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)  
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
 DE DNA binding protein homolog (Fragment).  
 OS Xestia c-nigrum granulosis virus (XngV) (Xestia c-nigrum  
 OS granulovirus).  
 OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae; Granulovirus.  
 OX NCB1\_TaxID=51677;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=alpha-4;  
 RX MEDLINE=98271593; PubMed=9608666;  
 RA Goto C., Hayakawa T., Maeda S.;  
 RT "Genome organization of Xestia c-nigrum granulovirus.";  
 RL Virus Genes 16:199-210(1998).  
 DR EMBL; U70897; AAB46487.1; -.  
 FT NON TER 1  
 SQ SEQUENCE 11 AA; 1371 MW; 6F05444852C1E454 CRC64;  
 Query Match 19.5%; Score 24; DB 12; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 4e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 12 RRNH 15  
 |||||  
 DB 3 RRNH 6  
 RESULT 22  
 ID O9PS22 PRELIMINARY; PRT; 11 AA.  
 AC O9PS22;  
 DT 01-MAY-2000 (TReMBLrel. 13, Created)  
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
 DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)  
 DE Hydrin 1', VASOTOCINYL-GLY-LYS.  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;  
 OC Xenopodinae; Xenopus.  
 OX NCB1\_TaxID=8355;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=93200145; PubMed=8452872;

Iwamuro S., Hayashi H., Kikuyama S.;  
 "An additional arginine-vasotocin-related peptide, vasotocinyl-Gly-Lys, in Xenopus neurohypophysis";  
 Biochim. Biophys. Acta 1176:143-147(1993).  
 GO: GO:0005576; C:extracellular; IEA.  
 GO: GO:0005185; F:neurohypophyseal hormone activity; IEA.  
 InterPro: IPR000981; Neurohyp\_horm.  
 Pfam: PF00220; hoxmone4; 1.  
 PROSITE: PS00264; NEUROHYPOPHYS HORM; 1.  
 SEQUENCE 11 AA; 1238 MW; C05B57EB176EB456 CRC64;

Query Match 19.5%; Score 24; DB 13; Length 11;  
 Best Local Similarity 45.3%; Pred. No. 4e+03;  
 Matches 5; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

6 CLIPACRRNHK 16  
 1 CYIQNCPGCK 11

JLT 23

Q86V63 PRELIMINARY; PRT; 17 AA.

01-JUN-2003 (TREMBlrel. 24, Created)

01-JUN-2003 (TREMBlrel. 24, Last sequence update)

01-OCT-2003 (TREMBlrel. 25, Last annotation update)

Thyroid hormone beta 1 receptor (Fragment).

HTK-BETA>1.

Homo sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

NCBI\_TaxID=9606;

[1]

SEQUENCE FROM N.A.

MEDLINE=96064788; PubMed=7593432;

Ozata M., Suzuki S., Takeda T., Malkin D.G., Miyamoto T., Liu R.T.,

Suzuki N., Silverberg J.D., Daneman D., Degroot L.J.;

"Functional analysis of a proline to serine mutation in codon 453 of

the thyroid hormone receptor beta 1 gene";

J. Clin. Endocrinol. Metab. 80:3239-3245(1995).

EMBL; S80765; AAP32229.1; -

GO: GO:0004872; F:receptor activity; IEA.

Receptor.

NON\_TER 1

NON\_TER 17

SEQUENCE 17 AA; 1993 MW; 2CD7D41F852AB9D1 CRC64;

Query Match 19.5%; Score 24; DB 4; Length 17;

Best Local Similarity 42.9%; Pred. No. 5.8e+03;

Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

2 NWRCLLI 8

4 SWKCSRI 10

ULT 24

4C4

Q8B4C4 PRELIMINARY; PRT; 17 AA.

01-MAR-2003 (TREMBlrel. 23, Created)

01-MAR-2003 (TREMBlrel. 23, Last sequence update)

01-MAR-2003 (TREMBlrel. 23, Last annotation update)

Precore.

Hepatitis B virus.

Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.

NCBI\_TaxID=10407;

[1]\_TaxID=10407;

SEQUENCE FROM N.A.

Vaishali C., Acharya S.K., Panda S.K.;

"Cryptic Hepatitis B virus infection: analysis of the complete genomic

sequence of HBV from nine patients with seronegative viral

RT hepatitis";  
 RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AV161158; AAC12630.1; -  
 SQ SEQUENCE 17 AA; 1908 MW; 0863A9BF82802588 CRC64;

Query Match 19.5%; Score 24; DB 12; Length 17;

Best Local Similarity 66.7%; Pred. No. 5.8e+03;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 CLIPAC 11

Db 7 CLIIISC 12

RESULT 25

O78379

ID O78379 PRELIMINARY; PRT; 18 AA.

AC O78379;

DT 01-NOV-1998 (TREMBlrel. 08, Created)

DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)

DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)

DE Small ribosomal protein S12 (Fragment).

GN RPS12.

OS Theileria annulata.

OG Chloroplast.

OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileridae;

OC Theileria.

OX NCBI\_TaxID=5874;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Hissar;

RA Denny P., Preiser P., Williamson D., Wilson I.;

"Evidence for a single origin of the 35 kb plastid DNA in

Apicomplexans";

RL Protist 149:51-59(1998).

DR EMBL; Y11429; CAA72235.1; -

DR GO: GO:0009507; C:chloroplast; IEA.

DR GO: GO:0003735; F:structural constituent of ribosome; IEA.

KW Chloroplast; Ribosomal protein.

FT NON\_TER 1

SQ SEQUENCE 18 AA; 2331 MW; BBFFCC6E3C6037A CRC64;

Query Match 19.5%; Score 24; DB 8; Length 18;

Best Local Similarity 60.0%; Pred. No. 6.1e+03;

Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 15 HKKFC 19

Db 14 YKKYC 18

RESULT 26

Q9UWM9

ID Q9UWM9 PRELIMINARY; PRT; 19 AA.

AC Q9UWM9;

DT 01-MAY-2000 (TREMBlrel. 13, Created)

DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)

DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)

DE Arginine vasopressin-neurophysin II (Fragment).

GN AVP.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA MEDLINE=91123474; PubMed=1840604;

RA Ito M., Mori Y., Oiso Y., Saito H.;

"A single base substitution in the coding region for neurophysin II

associated with familial central diabetes insipidus.";

J. Clin. Invest. 87:725-728(1991).

DR EMBL; M63733; AAA69844.1; -

FT NON\_TER 19

SEQUENCE 19 AA; 1985 MW; 5PF5PCD7BD990451 CRC64;

Query Match 19.5%; Score 24; DB 4; Length 19;  
 Best Local Similarity 60.0%; Pred. No. 6.4e+03;  
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

7 LIPAC 11  
 :|||  
 :|||  
 5 MLPAC 9

ULT 27  
 MB5

Q9XMB5 PRELIMINARY; PRT; 19 AA.  
 Q9XMB5; 01-NOV-1999 (TrEMBLrel. 12, Created)  
 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
 01-JUN-2003 (TrEMBLrel. 12, Last annotation update)  
 ORF165 (Fragment).  
 Aegilops tauschii (Tausch's goatgrass) (Aegilops squarrosa).  
 Mitochondrion.  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;  
 Triticeae; Aegilops.  
 NCBI\_TaxID=37682;  
 [1]  
 SEQUENCE FROM N.A.  
 STRAIN=KU29;  
 Tsukamoto N., Asakura N., Takumi S., Mori N., Nakamura C.,  
 "The presence of paternal sub-genomic mitochondrial DNA copies in the  
 nucleus-cytoplasm hybrids of tetraploid wheat with the cytoplasm of  
 Aegilops squarrosa.";  
 Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.  
 EMBL; AF142479; AAD37354.1; -.  
 GO; GO:0005739; C:mitochondrion; IEA.  
 InterPro; IPR003319; YMF19.  
 Pfam; PF02326; YMF19; 1.  
 NON TER 19  
 SEQUENCE 19 AA; 2394 MW; F435DB3B595D3ADC CRC64;

Query Match 19.5%; Score 24; DB 8; Length 19;  
 Best Local Similarity 57.1%; Pred. No. 6.4e+03;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1 FNRCCCL 7  
 13 FFWICLL 19

ULT 28  
 1577

Q88577 PRELIMINARY; PRT; 12 AA.  
 Q88577; 01-NOV-1996 (TrEMBLrel. 01, Created)  
 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 Theiler's murine encephalomyelitis virus 5' flank and 5' end cds  
 (Fragment).  
 Theiler's encephalomyelitis virus.  
 Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;  
 Cardiovirus.  
 NCBI\_TaxID=12124;  
 [1]  
 SEQUENCE FROM N.A.  
 MEDLINE=92194426; PubMed=1548749;  
 Pritchard A.E., Calenoff M.A., Simpson S., Jensen K., Lipton H.L.;  
 "A single base deletion in the 5' noncoding region of Theiler's virus  
 attenuates neurovirulence.";  
 J. Virol. 66:1951-1958(1992).  
 EMBL; M80885; AAA73156.1; -.  
 NON TER 12

SQ SEQUENCE 12 AA; 1321 MW; F79B7D908E7B5871 CRC64;

Query Match 18.7%; Score 23; DB 12; Length 12;  
 Best Local Similarity 30.0%; Pred. No. 6.2e+03;  
 Matches 3; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 10 ACRNHKKFC 19  
 ||:|  
 ||:|  
 Db 2 ACKHGYDVC 11

RESULT 29  
 Q88578 PRELIMINARY; PRT; 12 AA.  
 AC Q88578; 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Theiler's murine encephalomyelitis virus 5' flank and 5' end cds  
 (Fragment).  
 OS Theiler's encephalomyelitis virus.  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;  
 Cardiovirus.  
 OX NCBI\_TaxID=12124;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=TO(B15);  
 RX MEDLINE=92194426; PubMed=1548749;  
 RA Pritchard A.E., Calenoff M.A., Simpson S., Jensen K., Lipton H.L.;  
 "A single base deletion in the 5' noncoding region of Theiler's virus  
 attenuates neurovirulence.";  
 J. Virol. 66:1951-1958(1992).  
 RL EMBL; M80886; AAA73157.1; -.  
 DR NON TER 12  
 FT NON TER 12  
 SQ SEQUENCE 12 AA; 1321 MW; F79B7D908E7B5871 CRC64;

Query Match 18.7%; Score 23; DB 12; Length 12;  
 Best Local Similarity 30.0%; Pred. No. 6.2e+03;  
 Matches 3; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 10 ACRNHKKFC 19  
 ||:|  
 ||:|  
 Db 2 ACKHGYDVC 11

RESULT 30  
 Q88579 PRELIMINARY; PRT; 12 AA.  
 AC Q88579; 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Theiler's murine encephalomyelitis virus 5' flank and 5' end cds  
 (Fragment).  
 OS Theiler's encephalomyelitis virus.  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;  
 Cardiovirus.  
 OX NCBI\_TaxID=12124;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=VL;  
 RX MEDLINE=92194426; PubMed=1548749;  
 RA Pritchard A.E., Calenoff M.A., Simpson S., Jensen K., Lipton H.L.;  
 "A single base deletion in the 5' noncoding region of Theiler's virus  
 attenuates neurovirulence.";  
 J. Virol. 66:1951-1958(1992).  
 RL EMBL; M80887; AAA73158.1; -.  
 DR NON TER 12  
 FT NON TER 12  
 SQ SEQUENCE 12 AA; 1321 MW; F79B7D908E7B5871 CRC64;

Query Match 18.7%; Score 23; DB 12; Length 12;  
 Best Local Similarity 30.0%; Pred. No. 6.2e+03;  
 Matches 3; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

10 ACRNHHKFC 19  
||: :  
2 ACKGYDVC 11

UT 31

575  
Q88575 PRELIMINARY; PRT; 12 AA.  
Q88575 01-NOV-1996 (TREMELrel. 01, Created)  
01-NOV-1996 (TREMELrel. 01, Last sequence update)  
01-DEC-2001 (TREMELrel. 19, Last annotation update)  
Theiler's murine encephalomyelitis virus 5' flank and 5' end cds  
(Fragment).  
Theiler's encephalomyelitis virus.  
Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;  
Cardiovirus.  
NCBI\_TaxID=12124;  
[1]  
SEQUENCE FROM N.A.  
STRAIN=FA;  
MEDLINE=92194426; PubMed=1548749;  
Pritchard A.E., Calenoff M.A., Simpson S., Jensen K., Lipton H.L.;  
"A single base deletion in the 5' noncoding region of Theiler's virus  
attenuates neurovirulence."  
J. Virol. 66:1951-1958(1992).  
EMBL; M80883; AAA73154.1; -.  
NON TER 12 12  
SEQUENCE 12 AA; 1321 MW; F79B7D908E7B5871 CRC64;

Query Match 18.7%; Score 23; DB 12; Length 12;

Best Local Similarity 30.0%; Pred. No. 6.2e+03;

Matches 3; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

10 ACRNHHKFC 19

||: :  
2 ACKGYDVC 11

UT 32

580  
Q88580 PRELIMINARY; PRT; 12 AA.  
Q88580 01-NOV-1996 (TREMELrel. 01, Created)  
01-NOV-1996 (TREMELrel. 01, Last sequence update)  
01-DEC-2001 (TREMELrel. 19, Last annotation update)  
Theiler's murine encephalomyelitis virus 5' flank and 5' end cds  
(Fragment).  
Theiler's encephalomyelitis virus.  
Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;  
Cardiovirus.  
NCBI\_TaxID=12124;  
[1]  
SEQUENCE FROM N.A.  
STRAIN=Vilyusik;  
MEDLINE=92194426; PubMed=1548749;  
Pritchard A.E., Calenoff M.A., Simpson S., Jensen K., Lipton H.L.;  
"A single base deletion in the 5' noncoding region of Theiler's virus  
attenuates neurovirulence."  
J. Virol. 66:1951-1958(1992).  
EMBL; M80888; AAA73159.1; -.  
NON TER 12 12  
SEQUENCE 12 AA; 1321 MW; F79B7D908E7B5871 CRC64;

Query Match 18.7%; Score 23; DB 12; Length 12;

Best Local Similarity 30.0%; Pred. No. 6.2e+03;

Matches 3; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

10 ACRNHHKFC 19

||: :  
2 ACKGYDVC 11

RESULT 33

Q88582 PRELIMINARY; PRT; 12 AA.  
Q88582 01-NOV-1996 (TREMELrel. 01, Created)  
01-NOV-1996 (TREMELrel. 01, Last sequence update)  
01-DEC-2001 (TREMELrel. 19, Last annotation update)  
Theiler's murine encephalomyelitis virus 5' flank and 5' end cds  
(Fragment).  
Theiler's encephalomyelitis virus.  
Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;  
Cardiovirus.  
NCBI\_TaxID=12124;  
[1]  
SEQUENCE FROM N.A.  
STRAIN=TO(Vale);  
MEDLINE=92194426; PubMed=1548749;  
Pritchard A.E., Calenoff M.A., Simpson S., Jensen K., Lipton H.L.;  
"A single base deletion in the 5' noncoding region of Theiler's virus  
attenuates neurovirulence."  
J. Virol. 66:1951-1958(1992).  
EMBL; M80890; AAA73161.1; -.  
NON TER 12 12  
SEQUENCE 12 AA; 1321 MW; F79B7D908E7B5871 CRC64;

Query Match 18.7%; Score 23; DB 12; Length 12;

Best Local Similarity 30.0%; Pred. No. 6.2e+03;

Matches 3; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 10 ACRNHHKFC 19

||: :  
2 ACKGYDVC 11

RESULT 34

Q88581 PRELIMINARY; PRT; 12 AA.  
Q88581 01-NOV-1996 (TREMELrel. 01, Created)  
01-NOV-1996 (TREMELrel. 01, Last sequence update)  
01-DEC-2001 (TREMELrel. 19, Last annotation update)  
Theiler's murine encephalomyelitis virus 5' flank and 5' end cds  
(Fragment).  
Theiler's encephalomyelitis virus.  
Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;  
Cardiovirus.  
NCBI\_TaxID=12124;  
[1]  
SEQUENCE FROM N.A.  
STRAIN=WW;  
MEDLINE=92194426; PubMed=1548749;  
Pritchard A.E., Calenoff M.A., Simpson S., Jensen K., Lipton H.L.;  
"A single base deletion in the 5' noncoding region of Theiler's virus  
attenuates neurovirulence."  
J. Virol. 66:1951-1958(1992).  
EMBL; M80889; AAA73160.1; -.  
NON TER 12 12  
SEQUENCE 12 AA; 1321 MW; F79B7D908E7B5871 CRC64;

Query Match 18.7%; Score 23; DB 12; Length 12;

Best Local Similarity 30.0%; Pred. No. 6.2e+03;

Matches 3; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 10 ACRNHHKFC 19

||: :  
2 ACKGYDVC 11

RESULT 35

Q88576 PRELIMINARY; PRT; 12 AA.  
Q88576 01-NOV-1996 (TREMELrel. 01, Created)  
01-NOV-1996 (TREMELrel. 01, Last sequence update)  
01-DEC-2001 (TREMELrel. 19, Last annotation update)  
Theiler's murine encephalomyelitis virus 5' flank and 5' end cds  
(Fragment).  
Theiler's encephalomyelitis virus.  
Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;  
Cardiovirus.  
NCBI\_TaxID=12124;  
[1]  
SEQUENCE FROM N.A.  
STRAIN=TO(Vale);  
MEDLINE=92194426; PubMed=1548749;  
Pritchard A.E., Calenoff M.A., Simpson S., Jensen K., Lipton H.L.;  
"A single base deletion in the 5' noncoding region of Theiler's virus  
attenuates neurovirulence."  
J. Virol. 66:1951-1958(1992).  
EMBL; M80883; AAA73154.1; -.  
NON TER 12 12  
SEQUENCE 12 AA; 1321 MW; F79B7D908E7B5871 CRC64;



01-NOV-1996 (TRENBLrel. 01, Created)  
01-NOV-1996 (TRENBLrel. 01, Last sequence update)  
01-DEC-2001 (TRENBLrel. 19, Last annotation update)  
Theiler's murine encephalomyelitis virus 5' flank and 5' end cds  
(Fragment).  
Theiler's encephalomyelitis virus.  
Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;  
Cardiovirus.  
NCBI\_TaxID=12124;  
[1]  
SEQUENCE FROM N.A.  
STRAIN=MHG;  
MEDLINE=92194426; PubMed=1548749;  
Pritchard A.E., Calenoff M.A, Simpson S., Jensen K., Lipton H.L.;  
"A single base deletion in the 5' noncoding region of Theiler's virus  
attenuates neurovirulence."  
J. Virol. 66:1951-1958(1992).  
EMBL; M80884; AAA73155.1; -.  
NON TER 12  
SEQUENCE 12 AA; 1321 MW; F79B7D908E7B5871 CRC64;  
Query Match 18.7%; Score 23; DB 12; Length 12;  
Best Local Similarity 30.0%; Pred.No. 6.2e+03;  
Matches 3; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
10 ACRNHHKFC 19  
|||:  
2 ACKGYDVC 11

arch completed: February 18, 2004, 06:28:48  
; time : 40 secs

GenCore version 5.1.6  
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protein - protein search, using sw model

1 on: February 18, 2004, 06:08:09 ; Search time 52 seconds  
(without alignments)  
103.239 Million cell updates/sec

le: US-09-806-376-1

fect score: 123

quence: 1 FNRCCLPACRHHKFC 19

ring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

arched: 1586107 seqs, 282547505 residues

tal number of hits satisfying chosen parameters: 430463

imum DB seq length: 0

ximum DB seq length: 19

st-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

tabase :

- 1: Genesep29Jan04:\*
- 2: Genesep1980s:\*
- 3: Genesep1990s:\*
- 4: Genesep2000s:\*
- 5: Genesep2001s:\*
- 6: Genesep2002s:\*
- 7: Genesep2003as:\*
- 8: Genesep2003bs:\*
- 9: Genesep2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

sult No.	Score	Query Match	Length	DB ID	Description
1	123	100.0	19	3	AA92227 Rho-conotoxin
2	95	77.2	15	3	AA92228 Rho-conotoxin
3	50	40.7	18	2	AA75280 A-lineage
4	50	40.7	18	2	AA75280 A-lineage
5	49	39.8	16	2	AA75275 A-lineage
6	49	39.8	16	2	AA75275 A-lineage
7	49	39.8	16	2	AA75275 A-lineage
8	49	39.8	16	2	AA75275 A-lineage
9	49	39.8	16	2	AA75275 A-lineage
10	49	39.8	16	2	AA75275 A-lineage
11	49	39.8	16	2	AA75275 A-lineage
12	49	39.8	16	2	AA75275 A-lineage
13	49	39.8	16	2	AA75275 A-lineage
14	49	39.8	16	2	AA75275 A-lineage
15	49	39.8	16	2	AA75275 A-lineage
16	49	39.8	16	2	AA75275 A-lineage
17	49	39.8	16	2	AA75275 A-lineage
18	49	39.8	16	2	AA75275 A-lineage
19	49	39.8	16	2	AA75275 A-lineage
20	49	39.8	16	2	AA75275 A-lineage
21	49	39.8	16	2	AA75275 A-lineage
22	49	39.8	16	2	AA75275 A-lineage
23	49	39.8	16	2	AA75275 A-lineage
24	49	39.8	16	2	AA75275 A-lineage
25	49	39.8	16	2	AA75275 A-lineage

26	44	35.8	16	2	AAW12753 A-lineage
27	44	35.8	16	2	AAW12753 A-lineage
28	44	35.8	16	2	AAW12753 A-lineage
29	44	35.8	16	2	AAW12753 A-lineage
30	44	35.8	16	2	AAW12753 A-lineage
31	44	35.8	16	2	AAW12753 A-lineage
32	44	35.8	16	2	AAW12753 A-lineage
33	44	35.8	16	2	AAW12753 A-lineage
34	44	35.8	16	2	AAW12753 A-lineage
35	44	35.8	16	2	AAW12753 A-lineage
36	44	35.8	16	2	AAW12753 A-lineage
37	44	35.8	16	2	AAW12753 A-lineage
38	44	35.8	16	2	AAW12753 A-lineage
39	44	35.8	16	2	AAW12753 A-lineage
40	44	35.8	16	2	AAW12753 A-lineage
41	44	35.8	16	2	AAW12753 A-lineage
42	44	35.8	16	2	AAW12753 A-lineage
43	44	35.8	16	2	AAW12753 A-lineage
44	44	35.8	16	2	AAW12753 A-lineage
45	44	35.8	16	2	AAW12753 A-lineage
46	44	35.8	16	2	AAW12753 A-lineage
47	44	35.8	16	2	AAW12753 A-lineage
48	44	35.8	16	2	AAW12753 A-lineage
49	44	35.8	16	2	AAW12753 A-lineage
50	44	35.8	16	2	AAW12753 A-lineage

ALIGNMENTS

RESULT 1

AA92227

ID AA92227 standard; peptide; 19 AA.

XX AC AA92227;

XX DT 10-AUG-2000 (first entry)

XX DE Rho-conotoxin peptide, rho-TIA.

XX KW Rho-conotoxin; alpha-1-adrenoreceptor; antagonist; hypotensive; cardiatic;

XX KW analgesic; antiarrhythmic; cytotostatic; nootropic; antiinflammatory.

XX OS Conus tulipa.

XX PH Key Location/Qualifiers

FT Disulfide-bond 5 /note= "involved in disulphide bond"

FT Disulfide-bond 6 /note= "involved in disulphide bond"

FT Disulfide-bond 11 /note= "involved in disulphide bond"

FT Disulfide-bond 19 /note= "involved in disulphide bond"

XX WO200020443-A1.

13-APR-2000.

01-OCT-1999; 99WO-AU0000843.

02-OCT-1998; 98AU-00006273.

(UYQU ) UNIV-QUEENSLAND.

Lewis RJ, Alewood PF, Sharpe IA;

WPI; 2000-303737/26.

Isolated rho-conotoxin peptide used for the treatment of urinary or cardiovascular conditions or diseases, mood disorders or for control of pain or inflammation comprises selective alpha1-adrenoreceptor antagonist activity.

Claim 2; Page 31; 47pp; English.

The rho-conotoxin peptide, rho-TIA, is isolated from the venom duct of the fish hunting cone snail Conus tulipa. It contains two disulphide bonds. The rho-conotoxin peptide has selective alpha-1-adrenoceptor antagonist activity. It can be used in a receptor binding assay to test the activity of a molecule as an antagonist of alpha-1-adrenoceptor activity. Rho-TIA is labeled, e.g. with radioactive isotope and used to identify molecules which act at the same site. Antibodies to rho-TIA are useful as therapeutic and diagnostic agents. Rho-conotoxin can be used for the treatment of or prophylaxis of a urinary system disease, e.g. prostatic hyperplasia, cardiovascular disease, e.g. arrhythmia, hypertension or coronary heart failure, a mood disorder, e.g. craving (e.g. smoking craving) and pain, e.g. chronic pain, neuropathic pain or inflammatory pain (all claimed)

Sequence 19 AA;

Query Match 100.0%; Score 123; DB 3; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.7e-09;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 FNRCCCLIPACRRNHKKFC 19  
|||||  
1 FNRCCCLIPACRRNHKKFC 19

SULT 2  
Y92228

AA92228 standard; peptide; 15 AA.

AA92228;

10-AUG-2000 (first entry)

Truncated, inactive rho-conotoxin peptide derivative.

Rho-conotoxin; alpha-1-adrenoceptor; antagonist; hypotensive; cardiant; analgesic; antiarrhythmic; cyostatic; nootropic; antiinflammatory.

Conus tulipa.  
Synthetic.

Key Location/Qualifiers  
Disulfide-bond 5 /note= "involved in disulphide bond"  
Disulfide-bond 6 /note= "involved in disulphide bond"  
Disulfide-bond 11 /note= "involved in disulphide bond"  
Disulfide-bond 19 /note= "involved in disulphide bond"

WO200020443-A1.

13-APR-2000.

01-OCT-1999; 99WO-AU000843.

02-OCT-1998; 98AU-00006273.

(UYQU ) UNIV QUEENSLAND.

Lewis RJ, Alewood PF, Sharpe IA;

WPI; 2000-303737/26.

Isolated rho-conotoxin peptide used for the treatment of urinary or cardiovascular conditions or diseases, mood disorders or for control of pain or inflammation comprises selective alpha-1-adrenoceptor antagonist activity.

Disclosure; Page 3; 47pp; English.

The rho-conotoxin peptide, rho-TIA (see AA92227), is isolated from the venom duct of the fish hunting cone snail Conus tulipa. It contains two disulphide bonds. The rho-conotoxin peptide has selective alpha-1-adrenoceptor antagonist activity. It can be used in a receptor binding assay to test the activity of a molecule as an antagonist of alpha-1-adrenoceptor activity. Rho-TIA is labeled, e.g. with radioactive isotope and used to identify molecules which act at the same site. Antibodies to rho-TIA are useful as therapeutic and diagnostic agents. Rho-conotoxin can be used for the treatment of or prophylaxis of a urinary system disease, e.g. prostatic hyperplasia, cardiovascular disease, e.g. arrhythmia, hypertension or coronary heart failure, a mood disorder, e.g. craving (e.g. smoking craving) and pain, e.g. chronic pain, neuropathic pain or inflammatory pain (all claimed)

Sequence 15 AA;

Query Match 77.2%; Score 95; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.5e-05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CCLIPACRRNHKKFC 19  
|||||  
DB 1 CCLIPACRRNHKKFC 15

RESULT 3

AA92228

ID AA92228 standard; peptide; 18 AA.

AC AA92228;

DT 22-DEC-1995 (first entry)

DE A-lineage conotoxin SL-1 peptide.

KW Alpha conotoxin; neuromuscular; synapse; signal transmission.

OS Conus sulcatus.

FH Key Location/Qualifiers

FT Misc-difference 7 /label= Pro or OTHER  
FT /note= "Hydroxyproline"

FT Misc-difference 14 /label= Pro or OTHER  
FT /note= "Hydroxyproline"

FT Modified-site 15 /note= "Glu, can form a peptide bond via either the alpha  
or gamma carboxyl group"

FT Modified-site 18 /note= "preferably amidated"

FT WO9511256-A1.

PN 27-APR-1995.

PD 19-OCT-1994; 94WO-US011927.

PP 19-OCT-1993; 93US-00137800.

XX (UTAH ) UNIV UTAH RES FOUND.

XX Olivera BM, Cruz LJ, Hillyard DR, McIntosh JM, Santos AD;

XX WPI; 1995-170189/22.

XX New A-lineage conotoxin peptide(s) - which inhibit synaptic transmission  
at the neuromuscular junction or are active against potassium or sodium  
channels.

XX Claim 1; Page 44; 66pp; English.

PS

The kappa-conotoxin, alpha conotoxin and alpha-like conotoxin peptides all belong to a group of peptides known as the A-lineage conotoxin peptides. The A lineage conotoxin peptides have a wide variety of pharmacological uses. The A-lineage conotoxin peptides claimed (AAR75264-R75293) are useful for the inhibition of synaptic transmission at neuromuscular junctions by blocking nicotinic acetyl choline receptors and they also have activity against voltage-gated Na and K channels

Sequence 18 AA;

Query Match 40.7%; Score 50; DB 2; Length 18;  
Best Local Similarity 46.7%; Pred. No. 11;  
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

5 CCLIPACRRNHKKFC 19

||| ||||| :  
3 CCSFPACKYRPEMC 17

SULT 4  
W12742

AAW12742 standard; peptide; 18 AA.

AAW12742;

25-MAR-2003 (revised)  
16-APR-1997 (first entry)

A-lineage conotoxin peptide SL-1.

Polymerase chain reaction; PCR; primer; amplify; conotoxin; Conus; inhibitor; synaptic transmission; neuromuscular junction; sodium channel; nicotinic acetylcholine receptor; potassium channel; muscle relaxant; myasthenia gravis; small cell lung cancer; therapy.

Conus sulcatus.

Key Location/Qualifiers

Modified-site 7 /note= "optionally hydroxylated"

Modified-site 14 /note= "optionally hydroxylated"

Modified-site 15 /note= "optionally hydroxylated"

Modified-site 18 /note= "optionally gamma-carboxylated"

Modified-site 18 /note= "amidated"

US5589340-A.

31-DEC-1996.

07-JUN-1995; 95US-00477383.

29-JUN-1993; 93US-00084848.

19-OCT-1993; 93US-00137800.

(UTAH ) UNIV UTAH RES FOUND.

Santos AD, Hillyard DR, McIntosh JM, Olivera BM, Cruz LJ;

WPI; 1997-076840/07.

Identifying nucleic acid encoding A-lineage conotoxin peptide(s) by amplification - uses primers corresponding to conserved regions in the signal sequence and 3'-untranslated regions, useful e.g. in treatment of small cell lung cancer.

Disclosure; Col 5; 36pp; English.

AAW12726-W12769 represent conotoxin peptides. This sequence represents the A-lineage conotoxin SL-1 peptide isolated from Conus sulcatus. These sequences are identified using the method of the invention. The method of

the invention is for identifying DNA encoding A-lineage conotoxin peptides by subjecting Conus nucleic acid to amplification with primer sequences (see AAR75714 and AAR75715). The primers are specific for the signal sequence and 3'-untranslated (3'UTR) regions of the conotoxin gene, which are highly homologous between conotoxins, and are therefore suitable sites for detection. A-lineage conotoxins include alpha-conotoxins, and kappa-conotoxins. Alpha-conotoxins are powerful inhibitors of synaptic transmission at the neuromuscular junction, and are usually nicotinic acetylcholine receptor blockers. Kappa-conotoxins act on the voltage sensitive sodium and potassium channels. The conotoxins identified can be used as muscle relaxants, in the diagnosis of myasthenia gravis, and for the treatment or diagnosis of small cell lung cancer. For the treatment of small cell lung cancer, the conotoxin peptides act by binding to the nicotinic receptors, and thereby blocking the nicotine/cytosine stimulated release of the mitogen 5-hydroxytryptamine. (Updated on 25-MAR-2003 to correct PF field.)

XX Sequence 18 AA;

Query Match 40.7%; Score 50; DB 2; Length 18;  
Best Local Similarity 46.7%; Pred. No. 11;  
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OY 5 CCLIPACRRNHKKFC 19

||| ||||| :  
3 CCSFPACKYRPEMC 17

RESULT 5

AAR75275  
ID AAR75275 standard; peptide; 16 AA.

XX AAR75275;

DT 27-AUG-2003 (revised)  
DT 21-DEC-1995 (first entry)

XX A-lineage conotoxin BN-2 peptide.

XX Conotoxin; neuromuscular; synapse; signal transmission; inhibitor.

XX Conus bandanus.

XX Key Location/Qualifiers

FT Misc-difference 6 /label= Pro or OTHER

FT /note= "Hydroxyproline"

FT Misc-difference 13

FT /label= Pro or OTHER

FT /note= "Hydroxyproline"

FT Modified-site 16

FT /note= "preferably amidated"

XX WO9511256-A1.

XX 27-APR-1995.

XX 19-OCT-1994; 94WO-US011927.

XX 19-OCT-1993; 93US-00137800.

XX (UTAH ) UNIV UTAH RES FOUND.

XX Olivera BM, Cruz LJ, Hillyard DR, McIntosh JM, Santos AD;

XX WPI; 1995-170189/22.

XX New A-lineage conotoxin peptide(s) - which inhibit synaptic transmission at the neuromuscular junction or are active against potassium or sodium channels.

XX Claim 1; Page 42; 66pp; English.

The kappa-conotoxin, alpha conotoxin and alpha-like conotoxin peptides all belong to a group of peptides known as the A-lineage conotoxin peptides. The A-lineage conotoxin peptides have a wide variety of pharmacological uses. The A-lineage conotoxin peptides claimed (AAR75264-R75293) are useful for the inhibition of synaptic transmission at neuromuscular junctions by blocking nicotinic acetyl choline receptors and they also have activity against voltage-gated Na and K channels. (Updated on 27-AUG-2003 to correct OS field.)

Sequence 16 AA;

Query Match 39.8%; Score 49; DB 2; Length 16;  
Best Local Similarity 46.7%; Pred. No. 13;  
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

5 CCLIPACRRNHKKFC 19  
||| ||| :| :|  
2 CCTHPACHVSHPELC 16

RESULT 6  
AAW24882  
AAW24882 standard; peptide; 16 AA.

AAW24882;

25-MAR-2003 (revised)  
15-OCT-1997 (first entry)

Predatory cone snail venom alpha-conotoxin BN-2.

Conotoxin; venom; predatory; cone snail; Conus; A-lineage; inhibitor; synaptic transmission; neuromuscular junction; block; alpha-conotoxin; nicotinic acetylcholine receptor; kappa-conotoxin; voltage-sensitive potassium CHANNEL; sodium channel.

Conus bandanus.

Key Location/Qualifiers  
Modified-site 6  
/note= "optionally may be 4Hyp"  
Modified-site 13  
/note= "optionally may be 4Hyp"  
Modified-site 16  
/note= "amidated C-terminus"

US5633347-A.

27-MAY-1997.

07-JUN-1995; 95US-00480750.

29-JUN-1993; 93US-00084848.

19-OCT-1993; 93US-00137800.

(UTAH ) UNIV UTAH RES FOUND.

Hillyard DR, Cruz LJ, McIntosh JM, Santos AO, Olivera BM;

WPI; 1997-309336/28.

New kappa-conotoxin peptide(s) - present in venom of fish-hunting cone snail.

Disclosure; Col 5; 37pp; English.

The peptides AAW24878-W24900 represent novel toxin peptides isolated from the venom of various predatory cone snails of the genus Conus. The peptides are A-lineage conotoxin peptides which fall into 3 groups dependent on their amino acid sequences: (i) alpha-3/5 have a core sequence CCXXCXXCXXC where X is any amino acid; (ii) alpha-4/7 have a core sequence CCXXCXXCXXCXXC; and (iii) kappa-7/2/1/3 have the core sequence CCXXCXXCXXCXXCXXC. The peptide presented here was isolated

CC from Conus bandanus and falls into the alpha-4/7 category. Alpha-conotoxin peptides are potent inhibitors of synaptic transmission at the neuromuscular junction by blocking nicotinic acetylcholine receptors, CC whereas kappa-conotoxins have activities against voltage-sensitive CC potassium or sodium channels. (Updated on 25-MAR-2003 to correct PF CC field.)

XX Sequence 16 AA;

Query Match 39.8%; Score 49; DB 2; Length 16;  
Best Local Similarity 46.7%; Pred. No. 13;  
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 5 CCLIPACRRNHKKFC 19  
||| ||| :| :|  
Db 2 CCTHPACHVSHPELC 16

RESULT 7  
AAW12737  
AAW12737 standard; peptide; 16 AA.

AAW12737;

25-MAR-2003 (revised)  
16-APR-1997 (first entry)

A-lineage conotoxin peptide BN-2.

Polymerase chain reaction; PCR; primer; amplify; conotoxin; Conus; inhibitor; synaptic transmission; neuromuscular junction; sodium channel; CC nicotinic acetylcholine receptor; potassium channel; muscle relaxant; CC myasthenia gravis; small cell lung cancer; therapy.

Conus bandanus.

Key Location/Qualifiers  
Modified-site 6  
/note= "optionally hydroxylated"  
Modified-site 13  
/note= "optionally hydroxylated"  
Modified-site 15  
/note= "amidated"

US5589340-A.

31-DEC-1996.

07-JUN-1995; 95US-00477383.

29-JUN-1993; 93US-00084848.

19-OCT-1993; 93US-00137800.

(UTAH ) UNIV UTAH RES FOUND.

Santos AD, Hillyard DR, McIntosh JM, Olivera BM, Cruz LJ;

WPI; 1997-076840/07.

Identifying nucleic acid encoding A-lineage conotoxin peptide(s) by amplification - uses primers corresponding to conserved regions in the signal sequence and 3'-untranslated regions, useful e.g. in treatment of small cell lung cancer.

Disclosure; Col 5; 36pp; English.

AAW12725-W12769 represent conotoxin peptides. This sequence represents the A-lineage conotoxin BN-2 peptide isolated from Conus bandanus. These sequences are identified using the method of the invention. The method of the invention is for identifying DNA encoding A-lineage conotoxin peptides by subjecting Conus nucleic acid to amplification with primer sequences (see AAR59714 and AAR59715). The primers are specific for the signal sequence and 3'-untranslated (3'UTR) regions of the conotoxin

gene, which are highly homologous between conotoxins, and are therefore suitable sites for detection. A-lineage conotoxins include alpha-conotoxins, and kappa-conotoxins. Alpha-conotoxins are powerful inhibitors of synaptic transmission at the neuromuscular junction, and are usually nicotinic acetylcholine receptor blockers. Kappa-conotoxins act on the voltage sensitive sodium and potassium channels. The conotoxins identified can be used as muscle relaxants, in the diagnosis of myasthenia gravis, and for the treatment or diagnosis of small cell lung cancer. For the treatment of small cell lung cancer, the conotoxin peptides act by binding to the nicotinic receptors, and thereby blocking the nicotine/cytosine stimulated release of the mitogen 5-hydroxytryptamine. (Updated on 25-MAR-2003 to correct PF field.)

Sequence 16 AA;

Query Match 39.8%; Score 49; DB 2; Length 16;  
 Best Local Similarity 46.7%; Pred. No. 13;  
 Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;  
 5 CCLIPACRRNHKKFC 19  
 || || || || || || ||  
 2 CCTHPACHVSHPELC 16

SULT 8  
 P60018  
 ABP60018 standard; peptide; 16 AA.

ABP60018;

24-FEB-2003 (first entry)

Alpha-conotoxin peptide Anl.1.

Alpha-conotoxin; cerebroprotective; analgesic; anticonvulsant; neuroleptic; antiparkinsonian; cytostatic; nootropic; neuroprotective; neuronal nicotinic acetylcholine receptor; nAChR; inhibitor; stroke; pain; cancer related pain; post-surgical pain; oral pain; referred trigeminal neuralgia; post-herpetic neuralgia; phantom limb pain; fibromyalgia; reflex sympathetic dystrophy; rheumatoid arthritis; inflammatory arthritis; reflex sympathetic dystrophy; neuropathic pain; epilepsy; nicotine addiction; neurogenic pain; Parkinson's disease; small cell lung carcinoma; Alzheimer's disease; nerve injury.

Conus anemone.

Key Location/Qualifiers  
 Modified-site 16  
 /note= "C-terminal amide"

WO200279236-A1.

10-OCT-2002.

28-MAR-2002; 2002WO-AU000411.

29-MAR-2001; 2001AU-00004094.

(LIVE/) LIVETT B.  
 (KHAL/) KHALIL Z.  
 (GAYL/) GAYLER K.  
 (DOWN/) DOWN J.

Livett B, Khalil Z, Gayler K, Down J;

WPI; 2003-103260/09.

New alpha-conotoxin-like peptides that inhibit the activity of neuronal nicotinic acetylcholine receptor, useful for treating stroke, pain, schizophrenia, Parkinson's disease, small cell lung carcinoma or Alzheimer's disease.

PS Claim 9; Page 57; 87pp; English.

XX The invention relates to an isolated alpha-conotoxin-like peptide sequence. The activity of peptides of the invention may be described as cerebroprotective, analgesic, anticonvulsant, neuroleptic, antiparkinsonian, cytostatic, nootropic and neuroprotective. Peptides of the invention are neuronal nicotinic acetylcholine receptor (nAChR) inhibitors. The alpha-conotoxin-like peptide is useful for treating a condition mediated by a neuronal nicotinic acetylcholine receptor, e.g. stroke, pain (e.g. cancer related pain, post-surgical pain, oral or dental pain, referred trigeminal neuralgia, post-herpetic neuralgia, phantom limb pain, fibromyalgia, reflex sympathetic dystrophy, pain associated with inflammatory conditions, rheumatoid arthritis or inflammatory arthritis, or pain resulting from conditions associated with neurogenic or neuropathic pain), epilepsy, nicotine addiction, schizophrenia, Parkinson's disease, small cell lung carcinoma, or Alzheimer's disease. The alpha-conotoxin-like peptide is also useful for accelerating recovery from nerve injury. The peptides are also useful as research reagents for investigating nicotinic acetylcholine receptor physiology and pharmacology. The current sequence represents an alpha-conotoxin peptide of the invention that has been designated Anl.1

XX Sequence 16 AA;

Query Match 39.8%; Score 49; DB 6; Length 16;  
 Best Local Similarity 46.7%; Pred. No. 13;  
 Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 5 CCLIPACRRNHKKFC 19  
 || || || || || || ||  
 Db 2 CCHPACVANNQDYC 16

RESULT 9

ABG99820  
 ID ABG99820 standard; peptide; 17 AA.

AC ABG99820;

XX 17-JAN-2003 (first entry)

XX Conus sp conotoxin-associated peptide SEQ ID 505.

DE Conotoxin; cone snail; analgesic; voltage-gated ion channel modulator;  
 KW ligand-gated ion channel modulator; pain-relief.

XX Conus bandanus.

XX WO200264740-A2.

XX 22-AUG-2002.

XX 11-FEB-2002; 2002WO-US003887.

XX 09-FEB-2001; 2001US-0267408P.

XX (COGN-) COGNETIX INC.

PA (UTAH ) UNIV UTAH RES FOUND.

XX Olivera BM, McIntosh JM, Watkins M, Garrett JE, Cruz LJ;

PI Grilley M, Walker CS, Shetty R, Jones RM, Schoenfeld RM;

XX WPI; 2002-706921/76.

XX New cone snail conotoxin peptides, useful as a pain reliever for  
 PT alleviating pain in an individual suffering from pain or who is about to  
 PT be subjected to a pain-causing event, or for treating voltage-gated ion  
 PT channel disorders.

XX Claim 1; Page 298-299; 305pp; English.

XX This invention describes novel conotoxin peptides from the cone snail,  
 CC genus Conus which have analgesic activity and can act as a voltage-gated

ion channel modulator or a ligand-gated ion channel modulator. The conotoxin peptide is useful as a pain-relieving agent for alleviating pain in an individual who is either exhibiting pain or is about to be subjected to a pain-causing event. The conotoxin peptide is also useful for treating or preventing disorders associated with voltage-gated ion channel disorders, ligand-gated ion channel disorders or receptor disorders. The radiolabeled conotoxin peptide is also useful for characterizing a new site on these receptors or channels, and for screening and identifying novel small molecules that interact with the above-mentioned channels or receptors, which are monoamine transporters. ABG9360-ABG9983 represent the conotoxin protein and peptides described in the disclosure of the invention

Sequence 17 AA;

Query Match 39.8%; Score 49; DB 5; Length 17;  
Best Local Similarity 46.7%; Pred. No. 14;  
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

5 CCLIPACRRNHKKFC 19  
3 CCTHPACHVSHPELC 17

RESULT 10  
AB21436  
AAB21436 standard; peptide; 18 AA.

AAB21436;

19-JAN-2001 (first entry)

Cone snail alpha-conotoxin SEQ ID NO: 79.

Cone snail; alpha-conotoxin; venom; disulphide bond; mood disorder;  
neural nicotinic acetylcholine receptor; cardiovascular disorder;  
gastric motility disorder; urinary incontinence; nicotine addiction;  
small cell lung carcinoma.

Conus bandanus.

WO200044776-A1.

03-AUG-2000.

28-JAN-2000; 2000WO-US001579.

29-JAN-1999; 99US-0118381P.

(UTAH ) UNIV UTAH RES FOUND.  
(COGN-) COGNETIX INC.

Watkins M, Olivera BM, Hillyard DR, McIntosh JM, Jones RM;

WPI; 2000-505965/45.

N-PSDB; AAA89411.

alpha-conotoxin polypeptides derived from the venom of cone snails useful  
e.g. as neuromuscular blocking agents for use in surgery and for treating  
unipolar depression.

Claim 39; Page 34; 229pp; English.

The present invention relates to a number of alpha-conotoxin peptides and  
their coding sequences from a number of different species of cone snail.  
These peptides are found in minute quantities in the venom of the snails,  
and are targeted at the neuronal nicotinic acetylcholine receptors of the  
nervous system. They usually contain two disulphide bonds, which give  
them defined conformations, a rarity in molecules this small. The alpha-  
conotoxins can be used as neuromuscular blocking agents in surgery, and  
for treating disorders regulated at the neuronal nicotinic acetylcholine  
receptors, including cardiovascular disorders, gastric motility  
disorders, urinary incontinence, nicotine addiction, mood disorders such

CC as bipolar disorder, unipolar depression, dysthymia and seasonal  
CC affective disorder, and small cell lung carcinoma

XX Sequence 18 AA;

Query Match 39.8%; Score 49; DB 3; Length 18;  
Best Local Similarity 46.7%; Pred. No. 14;  
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 5 CCLIPACRRNHKKFC 19

Db 3 CCTHPACHVSHPELC 17

RESULT 11

AA24163

ID AAY24163 standard; peptide; 16 AA.

AC AAY24163;

XX 10-SEP-1999 (first entry)

XX Alpha-conotoxin peptide SEQ ID NO:9.

XX Alpha-conotoxin; neuronal nicotinic acetylcholine receptor; nAChR;  
small cell lung carcinoma; cardiovascular disorder; nicotine addiction;  
gastric motility disorder; urinary incontinence; mood disorder;  
bipolar disorder; unipolar depression; dysthymia;  
seasonal effective disorder.

XX Conus purpurascens.

XX WO9933482-A1.

XX 08-JUL-1999.

XX 23-DEC-1998; 98WO-US027367.

XX 31-DEC-1997; 97US-0070153P.

XX 03-APR-1998; 98US-0080588P.

XX (UTAH ) UNIV UTAH RES FOUND.

XX Olivera BM, McIntosh JM, Yoshikami D, Cartier GE, Luo S;

XX WPI; 1999-405367/34.

XX Alpha-conotoxin peptides that are used to treat disorders regulated at

XX neuronal nicotinic acetylcholine receptors.

XX Claim 28; Page 6; 40pp; English.

XX The present sequence represents a specifically claimed example of an  
XX alpha-conotoxin, which can be used to treat disorders regulated at  
XX neuronal nicotinic acetylcholine receptors (nAChR). The alpha-conotoxins  
XX are useful for preparing a pharmaceutical composition for treating  
XX disorders regulated at neuronal nAChR, especially alpha 3 beta 2, alpha 3  
XX beta 4 or alpha 7-containing nAChR. Disorders that can be treated include  
XX cardiovascular disorders, a gastric motility disorder, urinary  
XX incontinence, nicotine addiction, a mood disorder or small cell lung  
XX carcinoma. Mood disorders include bipolar disorder, unipolar depression,  
XX dysthymia and seasonal effective disorder. The alpha- conotoxins can also  
XX be used for diagnosis of small cell lung carcinoma. The alpha-conotoxin  
XX antagonists are able to discriminate between non- symmetrical ligand  
XX binding interfaces present on the nAChR. The alpha- conotoxin has the  
XX ability to potentially block any receptor containing a alpha beta subunit  
XX interface, regardless of what other subunits may be present in the  
XX receptor complex

XX Sequence 16 AA;

Query Match 39.0%; Score 48; DB 2; Length 16;

Best Local Similarity 40.0%; Pred. No. 17;

atches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

5 CCLIPACRRNHKKFC 19  
|||:|:|:|:  
2 CCSLPFCAANNPDYC 16

ULT 12  
424867

AAW24887 standard; peptide; 18 AA.

AAW24887;

25-MAR-2003 (revised)

15-OCT-1997 (first entry)

Predatory cone snail venom alpha-conotoxin SL-1.

Conotoxin; venom; predatory; cone snail; Conus; A-lineage; inhibitor;  
synaptic transmission; neuromuscular junction; block; alpha-conotoxin;  
nicotinic acetylcholine receptor; kappa-conotoxin;  
voltage-sensitive potassium CHANNEL; sodium channel.

Conus sulcatus.

Key Location/Qualifiers

Modified-site 7 /note= "optionally 4Hyp"

Modified-site 14 /note= "optionally 4Hyp"

Misc-difference 15

/label= Glu, OTHER

/note= "OTHER = gamma-carboxyglutamate (Glu)"

Modified-site 18 /note= "amidated C-terminus"

US5633347-A.

27-MAY-1997.

07-JUN-1995; 95US-00480750.

29-JUN-1993; 93US-00084848.

19-OCT-1993; 93US-00137800.

(UTAH ) UNIV UTAH RES FOUND.

Hillyard DR, Cruz LJ, McIntosh JM, Santos AO, Olivera BW;

WPI; 1997-309336/28.

New kappa-conotoxin peptide (s) - present in venom of fish-hunting cone snail.

Disclosure; Col 5; 37pp; English.

The peptides AAW24878-W4900 represent novel toxin peptides isolated from the venom of various predatory cone snails of the genus Conus. The peptides are A-lineage conotoxin peptides which fall into 3 groups dependent on their amino acid sequences: (i) alpha-3/5 have a core sequence CCXXXCCXXXCC where X is any amino acid; (ii) alpha-4/7 have a core sequence CCXXXCCXXXCC and (iii) kappa-7/2/1/3 have the core sequence CCXXXCCXXXCCXXXCC. The peptide presented here was isolated from Conus sulcatus and falls into the alpha-4/7 category. Alpha-conotoxin peptides are potent inhibitors of synaptic transmission at the neuromuscular junction by blocking nicotinic acetylcholine receptors, whereas kappa-conotoxins have activities against voltage-sensitive potassium or sodium channels. (Updated on 25-MAR-2003 to correct Pf field.)

Sequence 18 AA;

Query Match 39.0%; Score 48; DB 2; Length 18;

Best Local Similarity 46.7%; Pred. No. 19;  
Matches 7; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 5 CCLIPACRRNHKKFC 19  
|||:|:|:|:  
DB 3 CCSFPACRKVPXMC 17

RESULT 13

AAW87522

ID AAW87522 standard; peptide; 18 AA.

XX AC AAW87522;

XX DT 18-JUL-2000 (first entry)

XX DE Mature conotoxin peptide #2.

XX KW Mature conotoxin; brocade cone shell; line cone shell; drug screening;

XX KW neuronal inhibitor; muscle inhibitor.

XX OS Conus sp.

XX PN CN1237584-A.

XX PD 08-DEC-1999.

XX PF 30-APR-1999; 99CN-00106070.

XX PR 30-APR-1999; 99CN-00106070.

XX PA (BIOL-) BIOLOGICAL ENG INST ACAD MILITARY MEDICI.

XX PI Lu B, Huang P;

XX DR WPI; 2000-351193/31.

XX PT Conotoxin peptide from brocade cone shells useful as analgesic.

XX PS Claim 1A; Page 2; 20pp; Chinese.

XX CC The invention relates to 14 novel mature conotoxin peptides from marine snails (Conus species); conotoxin precursor proteins; and cDNAs encoding the conotoxin precursors. The mature peptide sequences were discovered by obtaining conotoxin cDNA sequences from mRNA from the brocade cone shell (Conus textile) or the line cone shell (Conus striatus). The cDNA sequences were used to determine the conotoxin precursor protein sequences, and the sequences of the mature conotoxin peptides were inferred from the precursor sequences. The mature conotoxin peptides can be obtained via chemical synthesis or by in vitro gene expression.

XX CC Conotoxins inhibit the function of neurons and muscle cells. Certain conotoxins interfere with synaptic transmission, while others act on muscle or at the neuromuscular junction. The 14 novel conotoxins have unique receptor specificity and affinity, so can be used as screening tools to identify new drugs. Conotoxin #11 (AAW87540) may be used for pain relief. Sequences AAW87420, AAW87522, AAW87524, AAW87526, AAW87528, AAW87530, AAW87532, AAW87534, AAW87536, AAW87538, AAW87540, AAW87542, AAW87544 and AAW87546 represent mature conotoxins #1-#14, respectively.

XX CC Sequence 18 AA;

XX SQ

Query Match 39.0%; Score 48; DB 3; Length 18;

Best Local Similarity 46.7%; Pred. No. 19;

Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 5 CCLIPACRRNHKKFC 19  
|||:|:|:|:  
DB 3 CCSHPACNVDHPEIC 17

RESULT 14

AAB21523

ID AAB21523 standard; peptide; 18 AA.



AA21523;

22-JAN-2001 (first entry)

Cone snail alpha-conotoxin SEQ ID NO: 203.

Cone snail; alpha-conotoxin; venom; disulphide bond; mood disorder; neuronal nicotinic acetylcholine receptor; cardiovascular disorder; gastric motility disorder; urinary incontinence; nicotine addiction; small cell lung carcinoma.

Conus musicus.

Key Location/Qualifiers

Misc-difference 2

/label= Lys, OTHER

/note= "N-methyl-Lys, N,N-dimethyl-Lys or N,N,N-trimethyl-Lys"

Misc-difference 12

/label= Lys, OTHER

/note= "N-methyl-Lys, N,N-dimethyl-Lys or N,N,N-trimethyl-Lys"

Misc-difference 14

/label= Pro, OTHER

/note= "hydroxy-Pro"

Misc-difference 16

/label= Tyr, OTHER

/note= "mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr or nitro-Tyr"

W020004776-A1.

03-AUG-2000.

28-JAN-2000; 2000WO-US001979.

29-JAN-1999; 99US-0118381P.

(UTAH ) UNIV UTAH RES FOUND.

(COGN-) COGNEX INC.

Watkins M, Olivera BM, Hillyard DR, McIntosh JM, Jones RM;

WPI; 2000-505965/45.

alpha-conotoxin polypeptides derived from the venom of cone snails useful e.g. as neuromuscular blocking agents for use in surgery and for treating unipolar depression.

Claim 21; Page 80; 229pp; English.

The present invention relates to a number of alpha-conotoxin peptides and their coding sequences from a number of different species of cone snail. These peptides are found in minute quantities in the venom of the snails, and are targeted at the neuronal nicotinic acetylcholine receptors of the nervous system. They usually contain two disulphide bonds, which give them defined conformations, a rarity in molecules this small. The alpha-conotoxins can be used as neuromuscular blocking agents in surgery, and for treating disorders regulated at the neuronal nicotinic acetylcholine receptors, including cardiovascular disorders, gastric motility disorders, urinary incontinence, nicotine addiction, mood disorders such as bipolar disorder, unipolar depression, dysthymia and seasonal affective disorder, and small cell lung carcinoma

Sequence 18 AA;

Query Match 39.0%; Score 48; DB 3; Length 18;

Best Local Similarity 46.7%; Pred. No. 19;

Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

5 CCLIPACRRNHKKFC 19

||: ||| | |

Db 3 CCINDACRSXHXQC 17

RESULT 15

AA24158

ID AA124158 standard; peptide; 16 AA.

XX AC

XX AAY24158;

XX DT 10-SEP-1999 (first entry)

XX DE

XX Alpha-conotoxin peptide SEQ ID NO:10.

XX KW

Alpha-conotoxin; neuronal nicotinic acetylcholine receptor; nAChR; small cell lung carcinoma; cardiovascular disorder; nicotine addiction;

KW gastric motility disorder; urinary incontinence; mood disorder;

KW bipolar disorder; unipolar depression; dysthymia;

XX seasonal effective disorder.

XX OS

Conus purpurascens.

XX Synthetic.

XX PN W09933482-A1.

XX PD 08-JUL-1999.

XX PF 23-DEC-1998; 98WO-US027367.

XX PR 31-DEC-1997; 97US-0070153P.

XX PR 03-APR-1998; 98US-008088P.

XX PA

(UTAH ) UNIV UTAH RES FOUND.

XX PI

Olivera BM, McIntosh JM, Yoshikami D, Cartier GE, Luo S;

XX DR WPI; 1999-405367/34.

XX PT

Alpha-conotoxin peptides that are used to treat disorders regulated at neuronal nicotinic acetylcholine receptors.

XX PS

Claim 12; Page 27; 40pp; English.

The present sequence represents a specifically claimed example of an alpha-conotoxin from the general formula given in AAY24155, which can be used to treat disorders regulated at neuronal nicotinic acetylcholine receptors (nAChR). The alpha-conotoxins are useful for preparing a pharmaceutical composition for treating disorders regulated at neuronal nAChR, especially alpha 3 beta 2, alpha 3 beta 4 or alpha 7-containing nAChR. Disorders that can be treated include cardiovascular disorders, a gastric motility disorder, urinary incontinence, nicotine addiction, a mood disorder or small cell lung carcinoma. Mood disorders include bipolar disorder, unipolar depression, dysthymia and seasonal effective disorder. The alpha-conotoxins can also be used for diagnosis of small cell lung carcinoma. The alpha-conotoxin antagonists are able to discriminate between non-symmetrical ligand binding interfaces present on the nAChR. The alpha-conotoxin has the ability to potentially block any receptor containing an alpha beta subunit interface, regardless of what other subunits may be present in the receptor complex

Sequence 16 AA;

Query Match 38.2%; Score 47; DB 2; Length 16;  
Best Local Similarity 40.0%; Pred. No. 23;  
Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

5 CCLIPACRRNHKKFC 19

||: ||| | |

2 CCLPPCALNNPDYC 16

||: ||| | |

5 CCLIPACRRNHKKFC 19

||: ||| | |

2 CCLPPCALNNPDYC 16

||: ||| | |

RESULT 16

AA21548

ID AA21548 standard; peptide; 17 AA.

AAE21548;  
 22-JAN-2001 (first entry)  
 Cone snail alpha-conotoxin SEQ ID NO: 228.  
 Cone snail; alpha-conotoxin; venom; disulphide bond; mood disorder;  
 neuronal nicotinic acetylcholine receptor; cardiovascular disorder;  
 gastric motility disorder; urinary incontinence; nicotine addiction;  
 small cell lung carcinoma.  
 Conus tulipa.  
 Key Location/Qualifiers  
 Misc-difference 6  
 /label= Pro, OTHER  
 /note= "hydroxy-Pro"  
 WO200044776-A1.  
 03-AUG-2000.  
 28-JAN-2000; 2000WO-US001979.  
 29-JAN-1999; 99US-0118381P.  
 (UTAH ) UNIV UTAH RES FOUND.  
 (COGN-) COGNETIX INC.  
 Watkins M, Olivera BM, Hillyard DR, McIntosh JM, Jones RM;  
 WPI; 2000-505965/45.  
 alpha-conotoxin polypeptides derived from the venom of cone snails useful  
 e.g. as neuromuscular blocking agents for use in surgery and for treating  
 unipolar depression.  
 Claim 21; Page 82; 229pp; English.  
 The present invention relates to a number of alpha-conotoxin peptides and  
 their coding sequences from a number of different species of cone snail.  
 These peptides are found in minute quantities in the venom of the snails,  
 and are targeted at the neuronal nicotinic acetylcholine receptors of the  
 nervous system. They usually contain two disulphide bonds, which give  
 them defined conformations, a rarity in molecules this small. The alpha-  
 conotoxins can be used as neuromuscular blocking agents in surgery, and  
 for treating disorders regulated at the neuronal nicotinic acetylcholine  
 receptors, including cardiovascular disorders, gastric motility  
 disorders, urinary incontinence, nicotine addiction, mood disorders such  
 as bipolar disorder, unipolar depression, dysthymia and seasonal  
 affective disorder, and small cell lung carcinoma  
 Sequence 17 AA;  
 Query Match 38.28; Score 47; DB 3; Length 17;  
 Best Local Similarity 53.34; Pred. No. 25;  
 Matches 8; Conservative 1; Mismatches 6; Indels 0; Gaps 0;  
 5 CCLIPACRRNHKFC 19  
 ||||| :||  
 2 CCSNXACLVNHRFC 16  
 RESULT 17  
 UR75292  
 AAR75292 standard; peptide; 18 AA.  
 AAR75292;  
 22-DEC-1995 (first entry)  
 A-lineage conotoxin U008 peptide.

XX Conotoxin; neuromuscular; synapse; signal transmission; inhibitor.  
 KW Conus ermineus.  
 OS  
 XX Key Location/Qualifiers  
 FH Misc-difference 3  
 FT /label= Pro or OTHER  
 FT /note= "Hydroxyproline"  
 FT Modified-site 18  
 FT /notes "preferably amidated"  
 XX WO9511256-A1.  
 BN  
 XX 27-APR-1995.  
 PD  
 XX 19-OCT-1994; 94WO-US011927.  
 PF  
 XX 19-OCT-1993; 93US-00137800.  
 PR  
 XX (UTAH ) UNIV UTAH RES FOUND.  
 PA  
 XX Olivera BM, Cruz LJ, Hillyard DR, McIntosh JM, Santos AD;  
 PI WPI; 1995-170189/22.  
 XX New A-lineage conotoxin peptide(s) - which inhibit synaptic transmission  
 PT at the neuromuscular junction or are active against potassium or sodium  
 PT channels.  
 XX Claim 1; Page 49; 66pp; English.  
 PS  
 XX The kappa-conotoxin, alpha conotoxin and alpha-like conotoxin peptides  
 CC all belong to a group of peptides known as the A-lineage conotoxin  
 CC peptides. The A-lineage conotoxin peptides have a wide variety of  
 CC pharmacological uses. The A-lineage conotoxin peptides claimed (AAR75264-  
 CC R75293) are useful for the inhibition of synaptic transmission at  
 CC neuromuscular junctions by blocking nicotinic acetyl choline receptors  
 CC and they also have activity against voltage-gated Na and K channels  
 XX Sequence 18 AA;  
 SQ  
 Query Match 37.44; Score 46; DB 2; Length 18;  
 Best Local Similarity 46.74; Pred. No. 35;  
 Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;  
 QY 5 CCLIPACRRNHKFC 19  
 ||||| :||  
 4 CCSNPACNVNHPQIC 18  
 Db  
 RESULT 18  
 AAW24897  
 ID AAW24897 standard; peptide; 18 AA.  
 XX  
 AC AAW24897;  
 XX 25-MAR-2003 (revised)  
 DT 15-OCT-1997 (first entry)  
 XX  
 DE Predatory cone snail venom alpha-conotoxin U008.  
 XX  
 KW Conotoxin; venom; predatory; cone snail; Conus; A-lineage; inhibitor;  
 KW synaptic transmission; neuromuscular junction; block; alpha-conotoxin;  
 KW nicotinic acetylcholine receptor; kappa-conotoxin;  
 KW voltage-sensitive potassium CHANNEL; sodium channel.  
 XX Conus ermineus.  
 OS  
 XX Key Location/Qualifiers  
 FH Modified-site 3  
 FT /note= "optionally may be dHyp"  
 FT Modified-site 18

/note= "amidated C-terminus"

US5633347-A.

27-MAY-1997.

07-JUN-1995; 95US-00480750.

29-JUN-1993; 93US-00084848.

19-OCT-1993; 93US-00137800.

(UTAH ) UNIV UTAH RES FOUND.

Hillyard DR, Cruz LJ, McIntosh JM, Santos AO, Olivera BM;

WPI; 1997-309336/28.

New kappa-conotoxin peptide(s) - present in venom of fish-hunting cone snail.

Disclosure; Col 6; 37pp; English.

The peptides AAW24878-W24900 represent novel toxin peptides isolated from the venom of various predatory cone snails of the genus *Conus*. The peptides are A-lineage conotoxin peptides which fall into 3 groups dependent on their amino acid sequences: (i) alpha-3/5 have a core sequence CXXXCXXXXC where X is any amino acid, (ii) alpha-4/7 have a core sequence CXXXCXXXCXXXC, and (iii) kappa-7/21/3 have the core sequence CXXXCXXXCXXXCXXXC. The peptide presented here was isolated from *Conus ermineus* and falls into the alpha-4/7 category. Alpha-conotoxin peptides are potent inhibitors of synaptic transmission at the neuromuscular junction by blocking nicotinic acetylcholine receptors, whereas kappa-conotoxins have activities against voltage-sensitive potassium or sodium channels. (Updated on 25-MAR-2003 to correct PF field.)

Sequence 18 AA;

Query Match 37.4%; Score 46; DB 2; Length 18;

Best Local Similarity 46.7%; Pred. No. 35;

Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

5 CCLIPACRRNHKKFC 19

4 CCSNPACNVNPPQIC 18

RESULT 19

AAW12751 standard; peptide; 18 AA.

AAW12751;

27-AUG-2003 (revised)

25-MAR-2003 (revised)

16-APR-1997 (first entry)

A-lineage conotoxin peptide U008.

Polymerase chain reaction; PCR; primer; amplify; conotoxin; *Conus*; inhibitor; synaptic transmission; neuromuscular junction; sodium channel; nicotinic acetylcholine receptor; potassium channel; muscle relaxant; myasthenia gravis; small cell lung cancer; therapy.

Conus ermineus.

Key Location/Qualifiers

Modified-site 3

/note= "optionally hydroxylated"

Modified-site 18

/note= "amidated"

US5589340-A.

XX 31-DEC-1996.

XX 07-JUN-1995; 95US-00477383.

XX 29-JUN-1993; 93US-00084848.

XX 19-OCT-1993; 93US-00137800.

XX (UTAH ) UNIV UTAH RES FOUND.

XX Santos AD, Hillyard DR, McIntosh JM, Olivera BM, Cruz LJ;

XX WPI; 1997-076840/07.

Identifying nucleic acid encoding A-lineage conotoxin peptide(s) by amplification - uses primers corresponding to conserved regions in the signal sequence and 3'-untranslated regions, useful e.g. in treatment of small cell lung cancer.

XX Disclosure; Col 6; 36pp; English.

AAW12726-W12769 represent conotoxin peptides. This sequence represents the A-lineage conotoxin U008 peptide isolated from *Conus ermineus*. These sequences are identified using the method of the invention. The method of the invention is for identifying DNA encoding A-lineage conotoxin peptides by subjecting *Conus* nucleic acid to amplification with primer sequences (see AAW59714 and AAW59715). The primers are specific for the signal sequence and 3'-untranslated (3'UTR) regions of the conotoxin gene, which are highly homologous between conotoxins, and are therefore suitable sites for detection. A-lineage conotoxins include alpha-conotoxins, and kappa-conotoxins. Alpha-conotoxins are powerful inhibitors of synaptic transmission at the neuromuscular junction, and are usually nicotinic acetylcholine receptor blockers. Kappa-conotoxins act on the voltage sensitive sodium and potassium channels. The conotoxins identified can be used as muscle relaxants, in the diagnosis of myasthenia gravis, and for the treatment or diagnosis of small cell lung cancer. For the treatment of small cell lung cancer, the conotoxin peptides act by binding to the nicotinic receptors, and thereby blocking the nicotine/cytosine stimulated release of the mitogen 5-hydroxytryptamine. (Updated on 25-MAR-2003 to correct PF field.) (Updated on 27-AUG-2003 to correct OS field.)

XX Sequence 18 AA;

Query Match 37.4%; Score 46; DB 2; Length 18;

Best Local Similarity 46.7%; Pred. No. 35;

Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 5 CCLIPACRRNHKKFC 19

Db 4 CCSNPACNVNPPQIC 18

RESULT 20

ABG99823

ID ABG99823 standard; peptide; 16 AA.

XX AC ABG99823;

XX 17-JAN-2003 (first entry)

XX Conus sp conotoxin-associated peptide SEQ ID 608.

Conotoxin; cone snail; analgesic; voltage-gated ion channel modulator; ligand-gated ion channel modulator; pain-relief.

XX Conus magus.

XX WO200264740-A2.

XX 22-AUG-2002.

XX 11-FEB-2002; 2002WO-US003887.

09-FEB-2001; 2001US-0267408P.

(COGN-) COGNETIX INC.  
(UTAH) UNIV UTAH RES FOUND.

Olivera BM, McIntosh JM, Watkins M, Garrett JE, Cruz LJ;  
Grille M, Walker CS, Shetty R, Jones RM, Schoenfeld RM;  
WPI; 2002-706921/76.

New cone snail conotoxin peptides, useful as a pain reliever for  
alleviating pain in an individual suffering from pain or who is about to  
be subjected to a pain-causing event, or for treating voltage-gated ion  
channel disorders.

Claim 1; Page 299; 305pp; English.

This invention describes novel conotoxin peptides from the cone snail,  
genus *Conus* which have analgesic activity and can act as a voltage-gated  
ion channel modulator or a ligand-gated ion channel modulator. The  
conotoxin peptide is useful as a pain-relieving agent for alleviating  
pain in an individual who is either exhibiting pain or is about to be  
subjected to a pain-causing event. The conotoxin peptide is also useful  
for treating or preventing disorders associated with voltage-gated ion  
channel disorders, ligand-gated ion channel disorders or receptor  
disorders. The radiolabeled conotoxin peptide is also useful for  
characterizing a new site on these receptors or channels, and for  
screening and identifying novel small molecules that interact with the  
above-mentioned channels or receptors, which are monoamine transporters.  
ABG93363-ABG99853 represent the conotoxin protein and peptides described  
in the disclosure of the invention

Sequence 16 AA;

Query Match 36.6%; Score 45; DB 5; Length 16;  
Best Local Similarity 40.0%; Pred. No. 42;  
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

5 CCLIPACRRNHKKFC 19  
|||  
2 CCVHPTCHLEHSLC 16

SULT 21  
187520

AA87520 standard; peptide; 18 AA.

AA87520;

18-JUL-2000 (first entry)

Mature conotoxin peptide #1.

Mature conotoxin; brocade cone shell; line cone shell; drug screening;  
neuronal inhibitor; muscle inhibitor.

*Conus* sp.

CN1237584-A.

08-DEC-1999.

30-APR-1999; 99CN-00106070.

30-APR-1999; 99CN-00106070.

(BIOL-) BIOLOGICAL ENG INST ACAD MILITARY MEDICI.

Lu B, Huang P;

WPI; 2000-351193/31.

Conotoxin peptide from brocade cone shells useful as analgesic.

Claim 1A; Page 2; 20pp; Chinese.

The invention relates to 14 novel mature conotoxin peptides from marine  
snails (*Conus* species); conotoxin precursor proteins; and cDNAs encoding  
the conotoxin precursors. The mature peptide sequences were discovered by  
obtaining conotoxin cDNA sequences from mRNA from the brocade cone shell  
(*Conus textile*) or the line cone shell (*Conus striatus*). The cDNA  
sequences were used to determine the conotoxin precursor protein  
sequences, and the sequences of the mature conotoxin peptides were  
inferred from the precursor sequences. The mature conotoxin peptides can  
be obtained via chemical synthesis or by in vitro gene expression.  
Conotoxins inhibit the function of neurons and muscle cells. Certain  
conotoxins interfere with synaptic transmission, while others act on  
muscle or at the neuromuscular junction. The 14 novel conotoxins have  
unique receptor specificity and affinity, so can be used as screening  
tools to identify new drugs. Conotoxin #11 (AA87540) may be used for  
pain relief. Sequences AA87420, AA87522, AA87524, AA87526, AA87528,  
AA87530, AA87532, AA87534, AA87536, AA87538, AA87540, AA87542,  
AA87544 and AA87546 represent mature conotoxins #1-#14, respectively  
SQ Sequence 18 AA;

Query Match 36.6%; Score 45; DB 3; Length 18;  
Best Local Similarity 40.0%; Pred. No. 47;  
Matches 6; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 5 CCLIPACRRNHKKFC 19  
|||  
Db 3 CCSDPRCNSHPELC 17

RESULT 22

AA875279

ID AA875279 standard; peptide; 16 AA.

AC AA875279;

XX 21-DEC-1995 (first entry)

DE A-lineage conotoxin MG-1 peptide.

Conotoxin; neuromuscular; synapse; signal transmission; inhibitor.

*Conus* magus.

Key Location/Qualifiers

Misc-difference 6

/label= Pro or OTHER

/note= "Hydroxyproline"

Modified-site 16

/note= "preferably amidated"

XX WO9511256-A1.

PN

XX 27-APR-1995.

XX 19-OCT-1994; 94WO-US011927.

XX 19-OCT-1993; 93US-00137800.

XX (UTAH) UNIV UTAH RES FOUND.

XX Olivera BM, Cruz LJ, Hillyard DR, McIntosh JM, Santos AD;

XX WPI; 1995-170189/22.

XX New A-lineage conotoxin peptide(s) - which inhibit synaptic transmission  
at the neuromuscular junction or are active against potassium or sodium  
channels.

XX Claim 1; Page 43; 66pp; English.

The kappa-conotoxin, alpha conotoxin and alpha-like conotoxin peptides all belong to a group of peptides known as the A-lineage conotoxin peptides. The A-lineage conotoxin peptides have a wide variety of pharmacological uses. The A-lineage conotoxin peptides claimed (AAW75264-R75293) are useful for the inhibition of synaptic transmission at neuromuscular junctions by blocking nicotinic acetylcholine receptors and they also have activity against voltage-gated Na and K channels and sequence 16 AA;

Query Match 35.8%; Score 44; DB 2; Length 16;  
 Best Local Similarity 40.0%; Pred. No. 57;  
 Matches 6; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

5 CCLIPACRRNHKKFC 19  
 |||||  
 2 CCSPNVCHEHSNLC 16

RESULT 23  
 AAW24886  
 AAW24886 standard; peptide; 16 AA.

AAW24886;

25-MAR-2003 (revised)  
 15-OCT-1997 (first entry)

Predatory cone snail venom alpha-conotoxin MG-1.

Conotoxin; venom; predatory; cone snail; Conus; A-lineage; inhibitor; synaptic transmission; neuromuscular junction; block; alpha-conotoxin; nicotinic acetylcholine receptor; kappa-conotoxin; voltage-sensitive potassium CHANNEL; sodium channel.

Conus magus.

Key Location/Qualifiers  
 Modified-site 16  
 /note= "optionally 4Hyp"

US5633347-A.  
 27-MAY-1997.

07-JUN-1995; 95US-00480750.  
 29-JUN-1993; 93US-00084848.  
 19-OCT-1993; 93US-00137800.

(UTAH ) UNIV UTAH RES FOUND.

Hillyard DR, Cruz LJ, McIntosh JM, Santos AO, Olivera BM; WPI; 1997-309336/28.

New kappa-conotoxin peptide(s) - present in venom of fish-hunting cone snail.

Disclosure; Col 5; 37pp; English.

The peptides AAW24878-W24900 represent novel toxin peptides isolated from the venom of various predatory cone snails of the genus Conus. The peptides are A-lineage conotoxin peptides which fall into 3 groups dependent on their amino acid sequences: (i) alpha-3/5 have a core sequence CXXXXXXXXC where X is any amino acid; (ii) alpha-4/7 have a core sequence CXXXXXXXXC and (iii) kappa-7/2/1/3 have the core sequence CXXXXXXXCXCCXXC. The peptide presented here was isolated from Conus magus and falls into the alpha-4/7 category. Alpha-conotoxin peptides are potent inhibitors of synaptic transmission at the neuromuscular junction by blocking nicotinic acetylcholine receptors, whereas kappa-conotoxins have activities against voltage-sensitive

potassium or sodium channels. (Updated on 25-MAR-2003 to correct PF field.)

Sequence 16 AA;

Query Match 35.8%; Score 44; DB 2; Length 16;  
 Best Local Similarity 40.0%; Pred. No. 57;  
 Matches 6; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

5 CCLIPACRRNHKKFC 19  
 |||||  
 2 CCSPNVCHEHSNLC 16

RESULT 24  
 AAW24899  
 AAW24899 standard; peptide; 16 AA.

AAW24899;

25-MAR-2003 (revised)  
 15-OCT-1997 (first entry)

Predatory cone snail venom alpha-conotoxin MII.

Conotoxin; venom; predatory; cone snail; Conus; A-lineage; inhibitor; synaptic transmission; neuromuscular junction; block; alpha-conotoxin; nicotinic acetylcholine receptor; kappa-conotoxin; voltage-sensitive potassium CHANNEL; sodium channel.

Conus magus.

Key Location/Qualifiers  
 Modified-site 16  
 /note= "amidated C-terminus"

US5633347-A.  
 27-MAY-1997.

07-JUN-1995; 95US-00480750.  
 29-JUN-1993; 93US-00084848.  
 19-OCT-1993; 93US-00137800.

(UTAH ) UNIV UTAH RES FOUND.

Hillyard DR, Cruz LJ, McIntosh JM, Santos AO, Olivera BM; WPI; 1997-309336/28.

New kappa-conotoxin peptide(s) - present in venom of fish-hunting cone snail.

Disclosure; Col 6; 37pp; English.

The peptides AAW24878-W24900 represent novel toxin peptides isolated from the venom of various predatory cone snails of the genus Conus. The peptides are A-lineage conotoxin peptides which fall into 3 groups dependent on their amino acid sequences: (i) alpha-3/5 have a core sequence CXXXXXXXXC where X is any amino acid; (ii) alpha-4/7 have a core sequence CXXXXXXXCXCCXXC; and (iii) kappa-7/2/1/3 have the core sequence CXXXXXXXCXCCXXC. The peptide presented here was isolated from Conus magus and falls into the alpha-4/7 category. Alpha-conotoxin peptides are potent inhibitors of synaptic transmission at the neuromuscular junction by blocking nicotinic acetylcholine receptors, whereas kappa-conotoxins have activities against voltage-sensitive potassium or sodium channels. (Updated on 25-MAR-2003 to correct PF field.)

Sequence 16 AA;

Query Match 35.8%; Score 44; DB 2; Length 16;

Best Local Similarity 40.0%; Pred. No. 57;  
Matches 6; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

5 CCLIPACRRNHKKFC 19  
|||  
2 CCNPFVCHLEHSLC 16

SULT 25  
WL2741

AAW12741 standard; peptide; 16 AA.

AAW12741;

25-MAR-2003 (revised)  
16-APR-1997 (first entry)

A-lineage conotoxin peptide MG-1.

Polymerase chain reaction; PCR; primer; amplify; conotoxin; Conus;  
inhibitor; synaptic transmission; neuromuscular junction; sodium channel;  
nicotinic acetylcholine receptor; potassium channel; muscle relaxant;  
myasthenia gravis; small cell lung cancer; therapy.

Conus magus.

Key Location/Qualifiers  
Modified-site 6 /note= "optionally hydroxylated"  
Modified-site 16 /note= "amidated"

US5589340-A.

31-DEC-1996.

07-JUN-1995; 95US-00477383.

29-JUN-1993; 93US-00084848.  
19-OCT-1993; 93US-00137800.

(UTAH ) UNIV UTAH RES FOUND.

Santos AD, Hillyard DR, McIntosh JM, Olivera BM, Cruz LJ;

WPI; 1997-076840/07.

Identifying nucleic acid encoding A-lineage conotoxin peptide(s) by  
amplification - uses primers corresponding to conserved regions in the  
signal sequence and 3'-untranslated regions, useful e.g. in treatment of  
small cell lung cancer.

Disclosure; Col 5; 36pp; English.

AAW12726-W12769 represent conotoxin peptides. This sequence represents  
the A-lineage conotoxin MG-1 peptide isolated from Conus magus. These  
sequences are identified using the method of the invention. The method of  
the invention is for identifying DNA encoding A-lineage conotoxin  
peptides by subjecting Conus nucleic acid to amplification with primer  
sequences (see AAT59714 and AAT59715). The primers are specific for the  
signal sequence and 3'-untranslated (3'UTR) regions of the conotoxin  
gene, which are highly homologous between conotoxins, and are therefore  
suitable sites for detection. A-lineage conotoxins include alpha-  
conotoxins, and kappa-conotoxins. Alpha-conotoxins are powerful  
inhibitors of synaptic transmission at the neuromuscular junction, and  
are usually nicotinic acetylcholine receptor blockers. Kappa-conotoxins  
act on the voltage sensitive sodium and potassium channels. The  
conotoxins identified can be used as muscle relaxants, in the diagnosis  
of myasthenia gravis, and for the treatment or diagnosis of small cell  
lung cancer. For the treatment of small cell lung cancer, the conotoxin  
peptides act by binding to the nicotinic receptors, and thereby blocking  
the nicotine/cytosine stimulated release of the mitogen 5-  
hydroxytryptamine. (Updated on 25-MAR-2003 to correct PF field.)

XX Sequence 16 AA;  
SQ

Query Match 35.8%; Score 44; DB 2; Length 16;  
Best Local Similarity 40.0%; Pred. No. 57;  
Matches 6; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 5 CCLIPACRRNHKKFC 19  
|||  
Db 2 CCNPFVCHLEHSLC 16

RESULT 26

AAW12753

ID AAW12753 standard; peptide; 16 AA.

XX AAW12753;

XX 25-MAR-2003 (revised)

DT 16-APR-1997 (first entry)

XX A-lineage conotoxin peptide MII.

XX Polymerase chain reaction; PCR; primer; amplify; conotoxin; Conus;  
KW inhibitor; synaptic transmission; neuromuscular junction; sodium channel;  
KW nicotinic acetylcholine receptor; potassium channel; muscle relaxant;  
KW myasthenia gravis; small cell lung cancer; therapy.

XX Conus magus.

XX Key Location/Qualifiers  
FH FT Modified-site 16  
FT /note= "amidated"

XX US5589340-A.

XX 31-DEC-1996.

XX 07-JUN-1995; 95US-00477383.

XX 29-JUN-1993; 93US-00084848.

XX 19-OCT-1993; 93US-00137800.

XX (UTAH ) UNIV UTAH RES FOUND.

XX Santos AD, Hillyard DR, McIntosh JM, Olivera BM, Cruz LJ;

XX WPI; 1997-076840/07.

XX Identifying nucleic acid encoding A-lineage conotoxin peptide(s) by  
PT amplification - uses primers corresponding to conserved regions in the  
PT signal sequence and 3'-untranslated regions, useful e.g. in treatment of  
PT small cell lung cancer.

XX Disclosure; Col 6; 36pp; English.

XX AAW12726-W12769 represent conotoxin peptides. This sequence represents  
CC the A-lineage conotoxin MII peptide isolated from Conus magus. These  
CC sequences are identified using the method of the invention. The method of  
CC the invention is for identifying DNA encoding A-lineage conotoxin  
CC peptides by subjecting Conus nucleic acid to amplification with primer  
CC sequences (see AAT59714 and AAT59715). The primers are specific for the  
CC signal sequence and 3'-untranslated (3'UTR) regions of the conotoxin  
CC gene, which are highly homologous between conotoxins, and are therefore  
CC suitable sites for detection. A-lineage conotoxins include alpha-  
CC conotoxins, and kappa-conotoxins. Alpha-conotoxins are powerful  
CC inhibitors of synaptic transmission at the neuromuscular junction, and  
CC are usually nicotinic acetylcholine receptor blockers. Kappa-conotoxins  
CC act on the voltage sensitive sodium and potassium channels. The  
CC conotoxins identified can be used as muscle relaxants, in the diagnosis  
CC of myasthenia gravis, and for the treatment or diagnosis of small cell  
CC lung cancer. For the treatment of small cell lung cancer, the conotoxin  
CC peptides act by binding to the nicotinic receptors, and thereby blocking  
CC the nicotine/cytosine stimulated release of the mitogen 5-  
CC hydroxytryptamine. (Updated on 25-MAR-2003 to correct PF field.)

the nicotine/cytosine stimulated release of the mitogen 5-hydroxytryptamine. (Updated on 25-MAR-2003 to correct PF field.)

Sequence 16 AA;

Query Match 35.8%; Score 44; DB 2; Length 16;  
Best Local Similarity 40.0%; Pred. No. 57;  
Matches 6; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

5 CCLIPACRRNHKKFC 19

2 CCSNPVCHLEHSNLC 16

RESULT 27

W57903  
AAW57903 standard; peptide; 16 AA.

AAW57903;

25-SEP-1998 (first entry)

Conotoxin peptide MII.

Conotoxin peptide; ImI; MII; cardiovascular agent; altered heart rate;  
altered blood pressure; nicotinic acetylcholine receptor antagonist;  
B neuron blocker; venom; marine snail; C neuron blocker;  
sympathetic impulse.

Conus imperialis.

Key Location/Qualifiers

Disulfide-bond 2: 8  
Disulfide-bond 3: 16

W09822126-A1.

28-MAY-1998.

17-NOV-1997; 97WO-US020669.

18-NOV-1996; 96US-0031141P.

(UTAH ) UNIV UTAH RES FOUND.

McIntosh JM, Olivera BM, Yoshikami D;

WPI; 1998-322346/28.

Use of the conotoxin peptide(s) ImI and MII - as agents which can regulate heart rate or blood pressure.

Claim 1; Page 4; 24pp; English.

This sequence represents the conotoxin peptide ImI. This sequence and the MII conotoxin peptide (see AAW57903) can be used in the method of the invention for the treatment of a patient who has an altered heart rate or an altered blood pressure. The peptides are found in the venom of marine snails of the genus Conus. They are active as nicotinic acetylcholine receptor antagonists. They differentially block the B and C neurons, and are thus able to differentially block sympathetic impulses to the heart affecting the heart rate and blood pressure. The above agents are capable of discretely affecting the heart rate or blood pressure, without affecting other muscles

Sequence 16 AA;

Query Match 35.8%; Score 44; DB 2; Length 16;  
Best Local Similarity 40.0%; Pred. No. 57;  
Matches 6; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

5 CCLIPACRRNHKKFC 19

Db 2 CCSNPVCHLEHSNLC 16

RESULT 28

AAW24167  
ID AAY24167 standard; peptide; 16 AA.

XX AC AAY24167;

XX 10-SEP-1999 (first entry)

XX Alpha-conotoxin peptide SEQ ID NO:2.

XX Alpha-conotoxin; neuronal nicotinic acetylcholine receptor; nAChR;  
small cell lung carcinoma; cardiovascular disorder; nicotine addiction;  
gastric motility disorder; urinary incontinence; mood disorder;  
bipolar disorder; unipolar depression; dysthymia;  
seasonal effective disorder.

XX Conus magus.

XX WO9933482-A1.

XX 08-JUL-1999.

XX 23-DEC-1998; 98WO-US027367.

XX 31-DEC-1997; 97US-0070153P.

XX 03-APR-1998; 98US-0080588P.

XX (UTAH ) UNIV UTAH RES FOUND.

XX Olivera BM, McIntosh JM, Yoshikami D, Cartier GE, Luo S;

XX WPI; 1999-405367/34.

XX Alpha-conotoxin peptides that are used to treat disorders regulated at neuronal nicotinic acetylcholine receptors.

XX Disclosure; Page 6; 40pp; English.

XX The present sequence represents an example of an alpha-conotoxin peptide, which can be used to treat disorders regulated at neuronal nicotinic acetylcholine receptors (nAChR). The alpha-conotoxins are useful for preparing a pharmaceutical composition for treating disorders regulated at neuronal nAChR, especially alpha 3 beta 2, alpha 3 beta 4 or alpha 7-containing nAChR. Disorders that can be treated include cardiovascular disorders, a gastric motility disorder, urinary incontinence, nicotine addiction, a mood disorder or small cell lung carcinoma. Mood disorders include bipolar disorder, unipolar depression, dysthymia and seasonal effective disorder. The alpha-conotoxins can also be used for diagnosis of small cell lung carcinoma. The alpha-conotoxin antagonists are able to discriminate between non-symmetrical ligand binding interfaces present on the nAChR. The alpha-conotoxin has the ability to potentially block any receptor containing an alpha beta subunit interface, regardless of what other subunits may be present in the receptor complex

XX Sequence 16 AA;

Query Match 35.8%; Score 44; DB 2; Length 16;

Best Local Similarity 40.0%; Pred. No. 57;

Matches 6; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 5 CCLIPACRRNHKKFC 19

Db 2 CCSNPVCHLEHSNLC 16

RESULT 29

AAW09520  
ID AAY09520 standard; peptide; 16 AA.

XX AC AAY09520;

20-JUL-1999 (first entry)  
 Alpha conopeptide MII SEQ ID NO:1.  
 Alpha conopeptide MII; alpha-4/7 conotoxin; cardiovascular agent;  
 neuronal nicotinic acetylcholine receptor; small cell lung carcinoma;  
 detection; gastric motility; urinary incontinence; anti-smoking agent.  
 Conus magus.  
 Key Location/Qualifiers  
 Disulfide-bond 2..8  
 Disulfide-bond 3..16  
 WO9921878-A1.  
 06-MAY-1999.  
 23-OCT-1998; 98WO-US022368.  
 24-OCT-1997; 97US-0062783P.  
 14-NOV-1997; 97US-0065814P.  
 (UTAH ) UNIV UTAH RES FOUND.  
 (UYCA-) UNIV CASE WESTERN RESERVE.  
 (SALK ) SALK INST.  
 (COGN-) COGNETIX INC.  
 Shon K. Olivera BM, Rivier JE, Koerber SC, Shen GS, McIntosh JW;  
 Cartier GE, Yoshikami D;  
 WPI; 1999-326697/27.  
 Derivatives of alpha-conotoxin and their analogs.  
 Example 11; Page 51; 176pp; English.  
 The present invention describes derivatives (I) of alpha-conotoxin MII  
 as (II), an alpha-4/7 conotoxin peptide, with practically the same activity  
 as (II). (I), and its mimetics, are useful as cardiovascular agents; for  
 treating or diagnosing small-cell lung carcinoma; and as gastric  
 motility, urinary incontinence and anti-smoking agents. (I) and their  
 mimetics can be designed to be selective for particular subtypes of  
 neuronal nicotinic acetylcholine receptor, particularly the alpha 3 beta  
 2 and alpha 3 beta 4 subtypes. The present sequence represents the alpha-  
 conopeptide MII, which is used in an example from the present invention  
 Q Sequence 16 AA;  
 Query Match 35.8%; Score 44; DB 2; Length 16;  
 Best Local Similarity 40.0%; Pred. No. 57;  
 Matches 6; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
 Y 5 CCLIPACRRNHKKFC 19  
 |||||  
 b 2 CCSNFCVCHLSNLC 16  
 RESULT 30  
 BG99827  
 D ABG99827 standard; peptide; 16 AA.  
 X  
 C ABG99827;  
 X  
 T 17-JAN-2003 (first entry)  
 X  
 E Conus sp conotoxin-associated peptide SEQ ID 612.  
 X  
 W Conotoxin; cone snail; analgesic; voltage-gated ion channel modulator;  
 W Ligand-gated ion channel modulator; pain-relief.  
 X  
 X Conus leopardus.  
 S

XX WO200264740-A2.  
 XX  
 XX 22-AUG-2002.  
 XX  
 XX 11-FEB-2002; 2002WO-US003887.  
 XX  
 XX 09-FEB-2001; 2001US-0267408P.  
 XX  
 XX (COGN-) COGNETIX INC.  
 XX (UTAH ) UNIV UTAH RES FOUND.  
 XX  
 XX Olivera BM, McIntosh JM, Watkins M, Garrett JE, Cruz LJ;  
 XX Grille M, Walker CS, Shetty R, Jones RM, Schoenfeld RM;  
 XX WPI; 2002-706921/76.  
 XX  
 XX New cone snail conotoxin peptides, useful as a pain reliever for  
 XX alleviating pain in an individual suffering from pain or who is about to  
 XX be subjected to a pain-causing event, or for treating voltage-gated ion  
 XX channel disorders.  
 XX  
 XX Claim 1; Page 300; 305pp; English.  
 XX  
 XX This invention describes novel conotoxin peptides from the cone snail,  
 XX genus Conus which have analgesic activity and can act as a voltage-gated  
 XX ion channel modulator or a ligand-gated ion channel modulator. The  
 XX conotoxin peptide is useful as a pain-relieving agent for alleviating  
 XX pain in an individual who is either exhibiting pain or is about to be  
 XX subjected to a pain-causing event. The conotoxin peptide is also useful  
 XX for treating or preventing disorders associated with voltage-gated ion  
 XX channel disorders, ligand-gated ion channel disorders or receptor  
 XX disorders. The radiolabeled conotoxin peptide is also useful for  
 XX characterizing a new site on these receptors or channels, and for  
 XX screening and identifying novel small molecules that interact with the  
 XX above-mentioned channels or receptors, which are monoamine transporters.  
 XX ABG9360-ABG9363 represent the conotoxin protein and peptides described  
 XX in the disclosure of the invention  
 XX  
 XX Sequence 16 AA;  
 Query Match 35.8%; Score 44; DB 5; Length 16;  
 Best Local Similarity 46.7%; Pred. No. 57;  
 Matches 7; Conservative 1; Mismatches 7; Indels 0; Gaps 0;  
 QY 5 CCLIPACRRNHKKFC 19  
 |||||  
 Db 1 CCSNFCVCHLSNLC 15  
 RESULT 31  
 ABP60014  
 ID ABP60014 standard; peptide; 16 AA.  
 XX  
 XX ABP60014;  
 AC  
 XX  
 XX 24-FEB-2003 (first entry)  
 DT  
 XX  
 XX Alpha-conotoxin peptide Vcl.1.  
 XX  
 XX Alpha-conotoxin; cerebroprotective; analgesic; anticonvulsant;  
 XX neuroleptic; antiparkinsonian; cytostatic; neuroprotective;  
 XX neuronal nicotinic acetylcholine receptor; nAChR; inhibitor; stroke;  
 XX pain; cancer related pain; post-surgical pain; oral pain;  
 XX referred trigeminal neuralgia; post-herpetic neuralgia;  
 XX phantom limb pain; fibromyalgia; reflex sympathetic dystrophy;  
 XX rheumatoid arthritis; inflammatory arthritis; neurogenic pain;  
 XX neuropathic pain; epilepsy; nicotine addiction; schizophrenia;  
 XX Parkinson's disease; small cell lung carcinoma; Alzheimer's disease;  
 XX nerve injury.  
 XX  
 XX Conus victorinae.  
 XX  
 XX Conus victorinae.  
 OS  
 XX



1 Key Location/Qualifiers  
 16  
 Modified-site /note= "C-terminal amide"  
 WO200279236-A1.  
 10-OCT-2002.  
 28-MAR-2002; 2002WO-AU000411.  
 29-MAR-2001; 2001AU-00004094.  
 (LIVE/) LIVETT B.  
 (KHALIL/) KHALIL Z.  
 (GAYLER/) GAYLER K.  
 (DOWN/) DOWN J.  
 Livett B, Khalil Z, Gayler K, Down J;  
 WPI; 2003-103260/09.  
 New alpha-conotoxin-like peptides that inhibit the activity of neuronal nicotinic acetylcholine receptor, useful for treating stroke, pain, schizophrenia, Parkinson's disease, small cell lung carcinoma or Alzheimer's disease.  
 Claim 8; Page 57; 87pp; English.  
 The invention relates to an isolated alpha-conotoxin-like peptide sequence. The activity of peptides of the invention may be described as cerebroprotective, analgesic, anticonvulsant, neuroleptic, antiparkinsonian, cytostatic, nontropic and neuroprotective. Peptides of the invention are neuronal nicotinic acetylcholine receptor (nAChR) inhibitors. The alpha-conotoxin-like peptide is useful for treating a condition mediated by a neuronal nicotinic acetylcholine receptor, e.g. stroke, pain (e.g. cancer related pain, post-surgical pain, oral or dental pain, referred trigeminal neuralgia, post-herpetic neuralgia, phantom limb pain, fibromyalgia, reflex sympathetic dystrophy, pain associated with inflammatory conditions, rheumatoid arthritis or inflammatory arthritis, or pain resulting from conditions associated with neurogenic or neuropathic pain), epilepsy, nicotine addiction, schizophrenia, Parkinson's disease, small cell lung carcinoma, or Alzheimer's disease. The alpha-conotoxin-like peptide is also useful for accelerating recovery from nerve injury. The peptides are also useful as research reagents for investigating nicotinic acetylcholine receptor physiology and pharmacology. The current sequence represents an alpha-conotoxin peptide of the invention that has been designated vcl.1  
 Sequence 16 AA;  
 Query Match 35.8%; Score 44; DB 6; Length 16;  
 Best Local Similarity 40.0%; Pred. No. 57;  
 Matches 6; Conservative 2; Mismatches 7; Indels 0; Gaps 0;  
 Y 5 CCLIPACRRNHKKFC 19  
 b 2 CCSDPRCNYDHPIC 16  
 RESULT 32  
 AY24156  
 D AAY24156 standard; peptide; 17 AA.  
 X C  
 C AAY24156;  
 X T  
 T 10-SEP-1999 (first entry)  
 X T  
 X Alpha-conotoxin peptide SEQ ID NO:3.  
 X Z  
 W Alpha-conotoxin; neuronal nicotinic acetylcholine receptor; nAChR;  
 W small cell lung carcinoma; cardiovascular disorder; nicotine addiction;  
 W gastric motility disorder; urinary incontinence; mood disorder;  
 W bipolar disorder; unipolar depression; dysthymia;

KW seasonal effective disorder.  
 XX Conus magus.  
 OS Synthetic.  
 XX WO9933482-A1.  
 XX 08-JUL-1999.  
 XX 23-DEC-1998; 98WO-US027367.  
 XX 31-DEC-1997; 97US-0070153P.  
 PR 03-APR-1998; 98US-0080588P.  
 XX (UTAH) UNIV UTAH RES FOUND.  
 XX Olivera BM, McIntosh JM, Yoshikami D, Cartier GE, Luo S;  
 WPI; 1999-405367/34.  
 XX Alpha-conotoxin peptides that are used to treat disorders regulated at neuronal nicotinic acetylcholine receptors.  
 PT Claim 12; Page 27; 40pp; English.  
 CC The present sequence represents a specifically claimed example of an alpha-conotoxin from the general formula given in AAY24155, which can be used to treat disorders regulated at neuronal nicotinic acetylcholine receptors (nAChR). The alpha-conotoxins are useful for preparing a pharmaceutical composition for treating disorders regulated at neuronal nAChR, especially alpha 3 beta 2, alpha 3 beta 4 or alpha 7-containing nAChR. Disorders that can be treated include cardiovascular disorders, a gastric motility disorder, urinary incontinence, nicotine addiction, a mood disorder or small cell lung carcinoma. Mood disorders include bipolar disorder, unipolar depression, dysthymia and seasonal affective disorder. The alpha-conotoxins can also be used for diagnosis of small cell lung carcinoma. The alpha-conotoxin antagonists are able to discriminate between non-symmetrical ligand binding interfaces present on the nAChR. The alpha-conotoxin has the ability to potentially block any receptor containing an alpha beta subunit interface, regardless of what other subunits may be present in the receptor complex  
 SQ Sequence 17 AA;  
 Query Match 35.8%; Score 44; DB 2; Length 17;  
 Best Local Similarity 40.0%; Pred. No. 60;  
 Matches 6; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
 QY 5 CCLIPACRRNHKKFC 19  
 Db 3 CCSPNVCVCHLEHSLC 17  
 RESULT 33  
 ABG99818  
 ID ABG99818 standard; peptide; 17 AA.  
 XX AC  
 AC ABG99818;  
 XX 17-JAN-2003 (first entry)  
 DT  
 DE Conus sp conotoxin-associated peptide SEQ ID 603.  
 XX  
 KW Conotoxin; cone snail; analgesic; voltage-gated ion channel modulator;  
 KW ligand-gated ion channel modulator; pain-relief.  
 XX Conus omaria.  
 OS  
 OS WO200264740-A2.  
 PN  
 PD 22-AUG-2002.  
 XX  
 XX 11-FEB-2002; 2002WO-US003887.



This invention describes novel conotoxin peptides from the cone snail, genus *Conus* which have analgesic activity and can act as a voltage-gated ion channel modulator or a ligand-gated ion channel modulator. The conotoxin peptide is useful as a pain-relieving agent for alleviating pain in an individual who is either exhibiting pain or is about to be subjected to a pain-causing event. The conotoxin peptide is also useful for treating or preventing disorders associated with voltage-gated ion channel disorders, ligand-gated ion channel disorders or receptor disorders. The radiolabeled conotoxin peptide is also useful for characterizing a new site on these receptors or channels, and for screening and identifying novel small molecules that interact with the above-mentioned channels or receptors, which are monoamine transporters. ABG99360-ABG99853 represent the conotoxin protein and peptides described in the disclosure of the invention

Sequence 17 AA;

Query Match 35.8%; Score 44; DB 5; Length 17;  
 Best Local Similarity 46.7%; Pred. NO. 60;  
 Matches 7; Conservative 1; Mismatches 7; Indels 0; Gaps 0;  
 5 CCLIPACRRNHKKFC 19  
 |||||  
 2 CCHPACVNVNPHIC 16

Search completed: February 18, 2004, 06:27:31  
 Time : 53 secs

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protein - protein search, using sw model  
on: February 18, 2004, 06:28:55 ; Search time 34 Seconds  
(without alignments)  
117.997 Million cell updates/sec

le: US-09-806-376-1  
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Gapop 10.0 , Gapext 0.5  
rched: 809742 seqs, 211153259 residues  
al number of hits satisfying chosen parameters: 181359  
imum DB seq length: 0  
imum DB seq length: 19

it-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 50 summaries

abase : Published Applications AA:\*  
1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep:\*  
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9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep:\*  
10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep:\*  
11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep:\*  
12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep:\*  
13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*  
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17: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB.pep:\*  
18: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

sult No.	Score	Query Match	Length	DB ID	Description
1	49	39.8	17	14	US-10-072-602B-605
2	48	39.0	16	9	US-09-897-465-9
3	47	38.2	16	9	US-09-897-465-10
4	45	36.6	16	14	US-10-072-602B-608
5	44	35.8	16	9	US-09-897-465-2
6	44	35.8	16	14	US-10-072-602B-612
7	44	35.8	17	14	US-09-897-465-3
8	44	35.8	17	14	US-10-072-602B-602
9	44	35.8	17	14	US-10-072-602B-603
10	44	35.8	17	14	US-10-072-602B-610
11	44	35.8	17	14	US-10-072-602B-618
12	43	35.0	16	9	US-09-897-465-11
13	43	35.0	19	10	US-09-910-009A-421
14	42	34.1	16	9	US-09-897-465-4
15	42	34.1	16	9	US-09-897-465-12

Sequence 606, App  
Sequence 613, App  
Sequence 440, App  
Sequence 21, Appl  
Sequence 607, App  
Sequence 5, Appl  
Sequence 6, Appl  
Sequence 410, App  
Sequence 604, App  
Sequence 113, App  
Sequence 113, App  
Sequence 615, App  
Sequence 8, Appl  
Sequence 34, Appl  
Sequence 609, App  
Sequence 346, App  
Sequence 170, App  
Sequence 171, App  
Sequence 172, App  
Sequence 442, App  
Sequence 429, App  
Sequence 58, Appl  
Sequence 166, App  
Sequence 621, App  
Sequence 11, Appl  
Sequence 403, App  
Sequence 417, App  
Sequence 404, App  
Sequence 150, App  
Sequence 398, App  
Sequence 105, App  
Sequence 102, App  
Sequence 108, App  
Sequence 112, App  
Sequence 159, App  
Sequence 170, App

ALIGNMENTS

RESULT 1  
US-10-072-602B-605  
; Sequence 605, Application US/10072602B  
; Publication No. US20030109670A1  
; GENERAL INFORMATION:  
; APPLICANT: University of Utah Research Foundation  
; APPLICANT: Cognetix, Inc.  
; APPLICANT: Olivera, Balomero M.  
; APPLICANT: McIntosh, J, Michael  
; APPLICANT: Watkins, Maren  
; APPLICANT: Garrett, James E.  
; APPLICANT: Cruz, Lourdes J.  
; APPLICANT: Grilley, Michelle  
; APPLICANT: Schoenfeld, Robert M.  
; APPLICANT: Walker, Craig  
; APPLICANT: Shetty, Reshma  
; APPLICANT: Jones, Robert M.  
; TITLE OF INVENTION: Cone Snail Peptides  
; FILE REFERENCE: 2314-249  
; CURRENT APPLICATION NUMBER: US/10072,602B  
; CURRENT FILING DATE: 2002-02-11  
; PRIOR APPLICATION NUMBER: US 60/267,408  
; PRIOR FILING DATE: 2001-02-09  
; NUMBER OF SEQ ID NOS: 638  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 605  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Conus bandanus  
US-10-072-602B-605

Query Match 39.8%; Score 49; DB 14; Length 17;  
Best Local Similarity 46.7%; Pred. No. 5.5;

Matches 7; Conservative 2; Mismatches 6; Indels 6; Gaps 0;  
5 CCLIPACRRNHKKFC 19  
|||:|:|  
3 CCTHPACHVSHPELC 17

Query Match 38.2%; Score 47; DB 9; Length 16;  
Best Local Similarity 40.0%; Pred. No. 9.7;  
Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;  
QY 5 CCLIPACRRNHKKFC 19  
|||:|:|:|  
DB 2 CCSLPPCALNNPDYC 16

## SULT 2

-09-897-465-9  
Sequence 9, Application US/09897465  
Patent No. US20020022715A1

GENERAL INFORMATION:  
APPLICANT: Olivera, Baldomero M.  
APPLICANT: McIntosh, J. Michael  
APPLICANT: Yoshikami, Doju  
APPLICANT: Cartier, G. Edward  
APPLICANT: Luo, Siqin  
TITLE OF INVENTION: Uses of Alpha-Conotoxin Peptides  
FILE REFERENCE: Uses of Alpha-Conotoxins  
CURRENT APPLICATION NUMBER: US/09/897,465  
CURRENT FILING DATE: 2001-07-03  
PRIOR APPLICATION NUMBER: US 60/080,588  
PRIOR FILING DATE: 1998-04-03  
PRIOR APPLICATION NUMBER: US 60/070,153  
PRIOR FILING DATE: 1997-12-31  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 9  
LENGTH: 16  
TYPE: PRT  
ORGANISM: Conus purpurascens  
-09-897-465-9

Query Match 39.0%; Score 48; DB 9; Length 16;  
Best Local Similarity 40.0%; Pred. No. 7.1;  
Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

5 CCLIPACRRNHKKFC 19  
|||:|:|:|  
2 CCSLPPCALNNPDYC 16

## SULT 3

-09-897-465-10  
Sequence 10, Application US/09897465  
Patent No. US20020022715A1

GENERAL INFORMATION:  
APPLICANT: Olivera, Baldomero M.  
APPLICANT: McIntosh, J. Michael  
APPLICANT: Yoshikami, Doju  
APPLICANT: Cartier, G. Edward  
APPLICANT: Luo, Siqin  
TITLE OF INVENTION: Uses of Alpha-Conotoxin Peptides  
FILE REFERENCE: Uses of Alpha-Conotoxins  
CURRENT APPLICATION NUMBER: US/09/897,465  
CURRENT FILING DATE: 2001-07-03  
PRIOR APPLICATION NUMBER: US 60/080,588  
PRIOR FILING DATE: 1998-04-03  
PRIOR APPLICATION NUMBER: US 60/070,153  
PRIOR FILING DATE: 1997-12-31  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 10  
LENGTH: 16  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: A10L derivative  
OTHER INFORMATION: of C. purpurascens PnIA  
-09-897-465-10

Query Match 36.6%; Score 45; DB 14; Length 16;  
Best Local Similarity 40.0%; Pred. No. 18;  
Matches 6; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 5 CCLIPACRRNHKKFC 19  
|||:|:|:|  
DB 2 CCYHPTCHLEHSLC 16

## RESULT 5

US-09-897-465-2  
Sequence 2, Application US/09897465  
Patent No. US20020022715A1  
GENERAL INFORMATION:  
APPLICANT: Olivera, Baldomero M.  
APPLICANT: McIntosh, J. Michael  
APPLICANT: Yoshikami, Doju  
APPLICANT: Cartier, G. Edward  
APPLICANT: Luo, Siqin  
TITLE OF INVENTION: Uses of Alpha-Conotoxin Peptides  
FILE REFERENCE: Uses of Alpha-Conotoxins  
CURRENT APPLICATION NUMBER: US/09/897,465  
CURRENT FILING DATE: 2001-07-03  
PRIOR APPLICATION NUMBER: US 60/080,588  
PRIOR FILING DATE: 1998-04-03  
PRIOR APPLICATION NUMBER: US 60/070,153  
PRIOR FILING DATE: 1997-12-31  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2  
LENGTH: 16  
TYPE: PRT



SULT 11  
-10-073-602B-618  
Sequence 618, Application US/10072602B  
Publication No. US20030109670A1  
GENERAL INFORMATION:  
APPLICANT: University of Utah Research Foundation  
APPLICANT: Cognetix, Inc.  
APPLICANT: Olivera, Baldomero M.

RESULT 13  
US-09-910-009A-42:

Sequence 421, Application US/09910009A  
Publication No. US20030050234A1  
GENERAL INFORMATION:  
APPLICANT: University of Utah Research Foundation  
APPLICANT: Cognetix, Inc.  
APPLICANT: Olivera, Baldomero M.  
APPLICANT: McIntosh, J. Michael  
APPLICANT: Garrett, James E.  
APPLICANT: Watkins, Maren  
APPLICANT: Cruz, Lourdes J.  
APPLICANT: Shon, Ki-Joon  
APPLICANT: Jacobsen, Richard  
APPLICANT: Jones, Robert M.  
APPLICANT: Cartier, G. Edward  
APPLICANT: Shen, Greg S.  
APPLICANT: Wagstaff, John D.  
TITLE OF INVENTION: Mu-Conopeptides  
FILE REFERENCE: 2314-242  
CURRENT APPLICATION NUMBER: US/09/910,009A  
CURRENT FILING DATE: 2001-07-23  
PRIOR APPLICATION NUMBER: US 60/219,619  
PRIOR FILING DATE: 2000-07-21  
PRIOR APPLICATION NUMBER: US 60/245,157  
PRIOR FILING DATE: 2000-11-03  
PRIOR APPLICATION NUMBER: US 60/264,319  
PRIOR FILING DATE: 2001-01-29  
PRIOR APPLICATION NUMBER: US 60/277,270  
PRIOR FILING DATE: 2001-03-21  
NUMBER OF SEQ ID NOS: 520  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 421  
LENGTH: 19  
TYPE: PR1  
ORGANISM: Conus marmoreus  
-09-910-009A-421

Query Match 35.0%; Score 43; DB 10; Length 19;  
Best Local Similarity 66.7%; Pred. No. 38;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
4 RCLIPACR 12  
: : : : :  
3 QCCHLPACR 11

SULT 14  
-09-897-465-4  
Sequence 4, Application US/09897465  
Patent No. US20020022715A1  
GENERAL INFORMATION:  
APPLICANT: Olivera, Baldomero M.  
APPLICANT: McIntosh, J. Michael  
APPLICANT: Yoshikami, Doju  
APPLICANT: Cartier, G. Edward  
APPLICANT: Luo, Siqin  
APPLICANT: University of Utah Research Foundation  
TITLE OF INVENTION: Uses of Alpha-Conotoxin Peptides  
FILE REFERENCE: Uses of Alpha-Conotoxins  
CURRENT APPLICATION NUMBER: US/09/897,465  
CURRENT FILING DATE: 2001-07-03  
PRIOR APPLICATION NUMBER: US 60/080,588  
PRIOR FILING DATE: 1998-04-03  
PRIOR APPLICATION NUMBER: US 60/070,153  
PRIOR FILING DATE: 1997-12-31  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 4  
LENGTH: 16  
TYPE: PR1  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: FAT derivative  
OTHER INFORMATION: of C. magus M11

US-09-897-465-4

Query Match 34.1%; Score 42; DB 9; Length 16;  
Best Local Similarity 40.0%; Pred. No. 45;  
Matches 6; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
QY 5 CCLIPACRRNHKKFC 19  
: : : : :  
DB 2 CCSPVCFATHSNLC 16

RESULT 15  
US-09-897-465-12  
Sequence 12, Application US/09897465  
Patent No. US20020022715A1  
GENERAL INFORMATION:  
APPLICANT: Olivera, Baldomero M.  
APPLICANT: McIntosh, J. Michael  
APPLICANT: Yoshikami, Doju  
APPLICANT: Cartier, G. Edward  
APPLICANT: Luo, Siqin  
APPLICANT: University of Utah Research Foundation  
TITLE OF INVENTION: Uses of Alpha-Conotoxins  
FILE REFERENCE: Uses of Alpha-Conotoxins  
CURRENT APPLICATION NUMBER: US/09/897,465  
CURRENT FILING DATE: 2001-07-03  
PRIOR APPLICATION NUMBER: US 60/080,588  
PRIOR FILING DATE: 1998-04-03  
PRIOR APPLICATION NUMBER: US 60/070,153  
PRIOR FILING DATE: 1997-12-31  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 12  
LENGTH: 16  
TYPE: PR1  
ORGANISM: Conus purpurascens  
US-09-897-465-12

Query Match 34.1%; Score 42; DB 9; Length 16;  
Best Local Similarity 33.3%; Pred. No. 45;  
Matches 5; Conservative 4; Mismatches 6; Indels 0; Gaps 0;  
QY 5 CCLIPACRRNHKKFC 19  
: : : : :  
DB 2 CCSPVCFATHSNLC 16

RESULT 16  
US-10-072-602B-606  
Sequence 606, Application US/10072602B  
Publication No. US20030109670A1  
GENERAL INFORMATION:  
APPLICANT: University of Utah Research Foundation  
APPLICANT: Cognetix, Inc.  
APPLICANT: Olivera, Baldomero M.  
APPLICANT: McIntosh, J. Michael  
APPLICANT: Watkins, Maren  
APPLICANT: Garrett, James E.  
APPLICANT: Cruz, Lourdes J.  
APPLICANT: Grilley, Michelle  
APPLICANT: Schoenfeld, Robert M.  
APPLICANT: Walker, Craig  
APPLICANT: Shetty, Reshma  
APPLICANT: Jones, Robert M.  
TITLE OF INVENTION: Cone Snail Peptides  
FILE REFERENCE: 2314-249  
CURRENT APPLICATION NUMBER: US/10/072,602B  
CURRENT FILING DATE: 2002-02-11  
PRIOR APPLICATION NUMBER: US 60/267,408  
PRIOR FILING DATE: 2001-02-09  
NUMBER OF SEQ ID NOS: 638  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 606



```
LENGTH: 17
TYPE: PRT
ORGANISM: Conus marmoreus
-10-072-602B-606

Query Match      34.1%; Score 42; DB 14; Length 17;
Best Local Similarity 40.0%; Pred. No. 47;
Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

5 CCLIPACRRNHKKFC 19
||| ||| : :
3 CCTHPACHVSNPGLC 17

SULT 17
-10-072-602B-613
Sequence 613, Application US/10072602B
Publication No. US20030109670A1
GENERAL INFORMATION:
APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Olivera, Baldomero M.
APPLICANT: McIntosh, J. Michael
APPLICANT: Watkins, Maren
APPLICANT: Garrett, James E.
APPLICANT: Cruz, Lourdes J.
APPLICANT: Grille, Michelle
APPLICANT: Schoenfeld, Robert M.
APPLICANT: Walker, Craig
APPLICANT: Shetty, Reshma
APPLICANT: Jones, Robert M.
TITLE OF INVENTION: Cone Snail Peptides
FILE REFERENCE: 2314-249
CURRENT APPLICATION NUMBER: US/10/072,602B
CURRENT FILING DATE: 2002-02-11
PRIOR APPLICATION NUMBER: US 60/267,408
PRIOR FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 638
SOFTWARE: PatentIn version 3.0
SEQ ID NO 613
LENGTH: 17
TYPE: PRT
ORGANISM: Conus emaciatu
-10-072-602B-613

Query Match      33.3%; Score 41; DB 14; Length 17;
Best Local Similarity 40.0%; Pred. No. 64;
Matches 6; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

5 CCLIPACRRNHKKFC 19
||| ||| : :
2 CCNFPACASNPGLC 16

SULT 18
-09-910-009A-440
Sequence 440, Application US/09910009A
Publication No. US20030050234A1
GENERAL INFORMATION:
APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Olivera, Baldomero M.
APPLICANT: McIntosh, J. Michael
APPLICANT: Garrett, James E.
APPLICANT: Watkins, Maren
APPLICANT: Cruz, Lourdes J.
APPLICANT: Shon, Ki-Joon
APPLICANT: Jacobsen, Richard
APPLICANT: Jones, Robert M.
APPLICANT: Cartier, G. Edward
APPLICANT: Shen, Greg S.
APPLICANT: Wagstaff, John D.
TITLE OF INVENTION: Mu-Conopeptides
```

```
FILE REFERENCE: 2314-242
CURRENT APPLICATION NUMBER: US/09/910,009A
CURRENT FILING DATE: 2001-07-23
PRIOR APPLICATION NUMBER: US 60/219,619
PRIOR FILING DATE: 2000-07-21
PRIOR APPLICATION NUMBER: US 60/245,157
PRIOR FILING DATE: 2000-11-03
PRIOR APPLICATION NUMBER: US 60/264,319
PRIOR FILING DATE: 2001-01-29
PRIOR APPLICATION NUMBER: US 60/277,270
PRIOR FILING DATE: 2001-03-21
NUMBER OF SEQ ID NOS: 520
SOFTWARE: PatentIn version 3.0
SEQ ID NO 440
LENGTH: 16
TYPE: PRT
ORGANISM: Conus marmoreus
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)..(16)
OTHER INFORMATION: Xaa is Hyp
US-09-910-009A-440

Query Match      31.7%; Score 39; DB 10; Length 16;
Best Local Similarity 71.4%; Pred. No. 11e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      5 CCLIPAC 11
||| |||
DB      2 CCXLPAC 8

RESULT 19
US-09-825-517A-21
Sequence 21, Application US/09825517A
Publication No. US20030203415A1
GENERAL INFORMATION:
APPLICANT: Rondon, Isaac J
APPLICANT: Ladner, Robert C
TITLE OF INVENTION: BINDING PEPTIDES FOR CARCINOEMBRYONIC
ANTIGEN (CEA)
FILE REFERENCE: DYX-016.1 (3421.1005-001)
CURRENT APPLICATION NUMBER: US/09/825,517A
CURRENT FILING DATE: 2003-03-24
PRIOR APPLICATION NUMBER: US 09/541,345
PRIOR FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 151
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 21
LENGTH: 16
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Isolate of TN10/9 library found not to bind CEA
US-09-825-517A-21

Query Match      31.7%; Score 39; DB 11; Length 16;
Best Local Similarity 75.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 NWRCCCLIP 9
||| |||
DB      1 NWRCKLFP 8

RESULT 20
US-10-072-602B-607
Sequence 607, Application US/10072602B
Publication No. US20030109670A1
GENERAL INFORMATION:
APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Olivera, Baldomero M.
```

APPLICANT: McIntosh, J. Michael  
APPLICANT: Watkins, Maren  
APPLICANT: Garrett, James E.  
APPLICANT: Cruz, Lourdes J.  
APPLICANT: Grilley, Michelle  
APPLICANT: Schoenfeld, Robert M.  
APPLICANT: Walker, Craig  
APPLICANT: Shetty, Reehma  
APPLICANT: Jones, Robert M.  
TITLE OF INVENTION: Cone Snail Peptides  
FILE REFERENCE: 2314-249  
CURRENT APPLICATION NUMBER: US/10/072,602B  
CURRENT FILING DATE: 2002-02-11  
PRIOR APPLICATION NUMBER: US 60/267,408  
PRIOR FILING DATE: 2001-02-09  
NUMBER OF SEQ ID NOS: 638  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 607  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Conus miles  
-10-072-602B-607

Query Match 30.9%; Score 38; DB 14; Length 15;  
Best Local Similarity 40.0%; Pred. No. 1.5e+02;  
Matches 6; Conservative 1; Mismatches 8; Indels 0; Gaps 0;  
5 CCLIPACRRNHKKFC 19  
1 CCNHPACAGKNSDLC 15

## SULT 21

-09-897-465-5  
Sequence 5, Application US/09897465  
Patent No. US20020022715A1  
GENERAL INFORMATION:  
APPLICANT: Olivera, Baldomero M.  
APPLICANT: McIntosh, J. Michael  
APPLICANT: Yoshikami, Doju  
APPLICANT: Cartier, G. Edward  
APPLICANT: Luo, Sigin  
APPLICANT: University of Utah Research Foundation  
TITLE OF INVENTION: Uses of Alpha-Conotoxin Peptides  
FILE REFERENCE: Uses of Alpha-Conotoxins  
CURRENT APPLICATION NUMBER: US/09/897,465  
CURRENT FILING DATE: 2001-07-03  
PRIOR APPLICATION NUMBER: US 60/080,588  
PRIOR FILING DATE: 1998-04-03  
PRIOR APPLICATION NUMBER: US 60/070,153  
PRIOR FILING DATE: 1997-12-31  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 5  
LENGTH: 16  
TYPE: PRT  
ORGANISM: Conus aulicus  
-09-897-465-5

Query Match 30.9%; Score 38; DB 9; Length 16;  
Best Local Similarity 33.3%; Pred. No. 1.5e+02;  
Matches 5; Conservative 2; Mismatches 8; Indels 0; Gaps 0;  
5 CCLIPACRRNHKKFC 19  
2 CC5YPPCFATNSDYC 16

## SULT 22

-09-897-465-6  
Sequence 6, Application US/09897465  
Patent No. US20020022715A1  
GENERAL INFORMATION:

APPLICANT: Olivera, Baldomero M.  
APPLICANT: McIntosh, J. Michael  
APPLICANT: Yoshikami, Doju  
APPLICANT: Cartier, G. Edward  
APPLICANT: Luo, Sigin  
APPLICANT: University of Utah Research Foundation  
TITLE OF INVENTION: Uses of Alpha-Conotoxin Peptides  
FILE REFERENCE: Uses of Alpha-Conotoxins  
CURRENT APPLICATION NUMBER: US/09/897,465  
CURRENT FILING DATE: 2001-07-03  
PRIOR APPLICATION NUMBER: US 60/080,588  
PRIOR FILING DATE: 1998-04-03  
PRIOR APPLICATION NUMBER: US 60/070,153  
PRIOR FILING DATE: 1997-12-31  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 6  
LENGTH: 17  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Tyr derivative  
OTHER INFORMATION: of C. aulicus AUIA  
US-09-897-465-6

Query Match 30.9%; Score 38; DB 9; Length 17;  
Best Local Similarity 33.3%; Pred. No. 1.6e+02;  
Matches 5; Conservative 2; Mismatches 8; Indels 0; Gaps 0;  
QY 5 CCLIPACRRNHKKFC 19  
DB 3 CC5YPPCFATNSDYC 17

## RESULT 23

US-10-072-602B-410  
Sequence 410, Application US/10072602B  
Publication No. US20030109670A1  
GENERAL INFORMATION:  
APPLICANT: University of Utah Research Foundation  
APPLICANT: Cognetix, Inc.  
APPLICANT: Olivera, Baldomero M.  
APPLICANT: McIntosh, J. Michael  
APPLICANT: Watkins, Maren  
APPLICANT: Garrett, James E.  
APPLICANT: Cruz, Lourdes J.  
APPLICANT: Grilley, Michelle  
APPLICANT: Schoenfeld, Robert M.  
APPLICANT: Walker, Craig  
APPLICANT: Shetty, Reehma  
APPLICANT: Jones, Robert M.  
TITLE OF INVENTION: Cone Snail Peptides  
FILE REFERENCE: 2314-249  
CURRENT APPLICATION NUMBER: US/10/072,602B  
CURRENT FILING DATE: 2002-02-11  
PRIOR APPLICATION NUMBER: US 60/267,408  
PRIOR FILING DATE: 2001-02-09  
NUMBER OF SEQ ID NOS: 638  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 410  
LENGTH: 17  
TYPE: PRT  
ORGANISM: Conus bandanus  
FEATURE:  
NAME/KEY: PEPTIDE  
LOCATION: (1)...(17)  
OTHER INFORMATION: Xaa at residues 2 and 15 is Glu or gamma-carboxy-Glu; Xaa at residues 1, 7 and 14 is Pro or hydroxy-Pro  
US-10-072-602B-410

Query Match 30.9%; Score 38; DB 14; Length 17;  
Best Local Similarity 40.0%; Pred. No. 1.6e+02;  
Matches 6; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

5 CCLIPACRRNHKFC 19  
3 CCTHXACHVSHXLC 17

SULT 24  
-10-072-602B-604  
Sequence 604, Application US/10072602B  
Publication No. US20030109670A1  
GENERAL INFORMATION:  
APPLICANT: University of Utah Research Foundation  
APPLICANT: Cognetix, Inc.  
APPLICANT: Olivera, Baldomero M.  
APPLICANT: McIntosh, J. Michael  
APPLICANT: Watkins, Maren  
APPLICANT: Garrett, James E.  
APPLICANT: Cruz, Lourdes J.  
APPLICANT: Grilley, Michelle  
APPLICANT: Schoenfeld, Robert M.  
APPLICANT: Walker, Craig  
APPLICANT: Shetty, Reshma  
APPLICANT: Jones, Robert M.  
TITLE OF INVENTION: Cone Snail Peptides  
FILE REFERENCE: 2314-249  
CURRENT APPLICATION NUMBER: US/10/072,602B  
CURRENT FILING DATE: 2002-02-11  
PRIOR APPLICATION NUMBER: US 60/267,408  
PRIOR FILING DATE: 2001-02-09  
NUMBER OF SEQ ID NOS: 638  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 604  
LENGTH: 19  
TYPE: PRT  
ORGANISM: Conus quercinus  
-10-072-602B-604  
Query Match 30.9%; Score 38; DB 14; Length 19;  
Best Local Similarity 40.0%; Pred. No. 1.8e+02;  
Matches 6; Conservative 2; Mismatches 7; Indels 0; Gaps 0;  
5 CCLIPACRRNHKFC 19  
3 CCSDPACAVSNPDIC 17  
SULT 25  
-09-908-741-113  
Sequence 113, Application US/09908741  
Publication No. US20030050435A1  
GENERAL INFORMATION:  
APPLICANT: Olivera, Baldomero M.  
APPLICANT: Laver, Richard T.  
APPLICANT: Watkins, Maren  
APPLICANT: Hillyard, David R.  
APPLICANT: McIntosh, J. Michael  
APPLICANT: Schoenfeld, Robert M.  
APPLICANT: Jones, Robert M.  
APPLICANT: Nielsen, Jake  
APPLICANT: University of Utah Research Foundation  
APPLICANT: Cognetix, Inc.  
TITLE OF INVENTION: Alpha Conotoxin Peptides  
FILE REFERENCE: Alpha CIP  
CURRENT APPLICATION NUMBER: US/09/908,741  
CURRENT FILING DATE: 2001-07-20  
PRIOR APPLICATION NUMBER: US 60/116,881  
PRIOR FILING DATE: 1999-01-22  
PRIOR APPLICATION NUMBER: US 60/116,882  
PRIOR FILING DATE: 1999-01-22  
PRIOR APPLICATION NUMBER: US 09/488,799  
PRIOR FILING DATE: 2000-01-21  
PRIOR APPLICATION NUMBER: US 60/219,407  
PRIOR FILING DATE: 2000-07-20

PRIOR APPLICATION NUMBER: US 60/221,557  
PRIOR FILING DATE: 2000-07-28  
NUMBER OF SEQ ID NOS: 125  
SOFTWARE: PatentIn ver. 2.0  
SEQ ID NO 113  
LENGTH: 14  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence.MI Analog  
US-09-908-741-113  
Query Match 30.5%; Score 37.5; DB 10; Length 14;  
Best Local Similarity 61.5%; Pred. No. 1.6e+02;  
Matches 8; Conservative 1; Mismatches 3; Indels 1; Gaps 1;  
QY 4 RCLIPACRRNHK 16  
DB 2 RCC-HPACQNTK 13  
RESULT 26  
US-10-072-602B-615  
Sequence 615, Application US/10072602B  
Publication No. US20030109670A1  
GENERAL INFORMATION:  
APPLICANT: University of Utah Research Foundation  
APPLICANT: Cognetix, Inc.  
APPLICANT: Olivera, Baldomero M.  
APPLICANT: McIntosh, J. Michael  
APPLICANT: Watkins, Maren  
APPLICANT: Garrett, James E.  
APPLICANT: Cruz, Lourdes J.  
APPLICANT: Grilley, Michelle  
APPLICANT: Schoenfeld, Robert M.  
APPLICANT: Walker, Craig  
APPLICANT: Shetty, Reshma  
APPLICANT: Jones, Robert M.  
TITLE OF INVENTION: Cone Snail Peptides  
FILE REFERENCE: 2314-249  
CURRENT APPLICATION NUMBER: US/10/072,602B  
CURRENT FILING DATE: 2002-02-11  
PRIOR APPLICATION NUMBER: US 60/267,408  
PRIOR FILING DATE: 2001-02-09  
NUMBER OF SEQ ID NOS: 638  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 615  
LENGTH: 17  
TYPE: PRT  
ORGANISM: Conus cinereus gubba  
US-10-072-602B-615  
Query Match 30.5%; Score 37.5; DB 14; Length 17;  
Best Local Similarity 46.7%; Pred. No. 1.9e+02;  
Matches 7; Conservative 1; Mismatches 6; Indels 1; Gaps 1;  
QY 5 CCLIPACRRNHKFC 19  
DB 3 CCSFPFCIANN-PFC 16  
RESULT 27  
US-09-897-465-8  
Sequence 8, Application US/09897465  
Patent No. US2002002715A1  
GENERAL INFORMATION:  
APPLICANT: Olivera, Baldomero M.  
APPLICANT: McIntosh, J. Michael  
APPLICANT: Yoshikami, Doju  
APPLICANT: Cartier, G. Edward  
APPLICANT: Luo, Siqin  
APPLICANT: University of Utah Research Foundation  
TITLE OF INVENTION: Uses of Alpha-Conotoxin Peptides

FILE REFERENCE: Uses of Alpha-Conotoxins  
CURRENT APPLICATION NUMBER: US/09/897,465  
CURRENT FILING DATE: 2001-07-03  
PRIOR APPLICATION NUMBER: US 60/080,588  
PRIOR FILING DATE: 1998-04-03  
PRIOR APPLICATION NUMBER: US 60/070,153  
PRIOR FILING DATE: 1997-12-31  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 8  
LENGTH: 16  
TYPE: PRT  
ORGANISM: Conus aulicus  
-09-897-465-8

Query Match 30.1%; Score 37; DB 9; Length 16;  
Best Local Similarity 33.3%; Pred. No. 2.1e+02;  
Matches 5; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

5 CCLIPACRRNHKKFC 19  
||| :  
2 CCGYPPTATNSGYC 16

SULT 28  
-10-196-394-34  
Sequence 34, Application US/10196394  
Publication No. US20030171278A1  
GENERAL INFORMATION:  
APPLICANT: Mark S. Dennis  
TITLE OF INVENTION: Compounds that Bind HER2  
FILE REFERENCE: P1713R1  
CURRENT APPLICATION NUMBER: US/10/196,394  
CURRENT FILING DATE: 2002-07-15  
PRIOR APPLICATION NUMBER: US/09/609,721  
PRIOR FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: US 60/142,232  
PRIOR FILING DATE: 1998-07-02  
NUMBER OF SEQ ID NOS: 162  
SEQ ID NO 34  
LENGTH: 16  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: synthetic peptide sequence  
-10-196-394-34

Query Match 30.1%; Score 37; DB 14; Length 16;  
Best Local Similarity 50.0%; Pred. No. 2.1e+02;  
Matches 7; Conservative 1; Mismatches 4; Indels 2; Gaps 1;

1 FNWR--CCLIPACR 12  
||| :  
1 FNWEKNGCIGPCR 14

SULT 29  
-10-072-602B-609  
Sequence 609, Application US/10072602B  
Publication No. US20030109670A1  
GENERAL INFORMATION:  
APPLICANT: University of Utah Research Foundation  
APPLICANT: Cognetix, Inc.  
APPLICANT: Olivera, Baldomero M.  
APPLICANT: McIntosh, J. Michael  
APPLICANT: Watkins, Maren  
APPLICANT: Garrett, James E.  
APPLICANT: Cruz, Lourdes J.  
APPLICANT: Grilley, Michelle  
APPLICANT: Schoenfeld, Robert M.  
APPLICANT: Walker, Craig  
APPLICANT: Shetty, Reshma  
APPLICANT: Jones, Robert M.

TITLE OF INVENTION: Cone Snail Peptides  
FILE REFERENCE: 2314-249  
CURRENT APPLICATION NUMBER: US/10/072,602B  
CURRENT FILING DATE: 2002-02-11  
PRIOR APPLICATION NUMBER: US 60/267,408  
PRIOR FILING DATE: 2001-02-09  
NUMBER OF SEQ ID NOS: 638  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 609  
LENGTH: 17  
TYPE: PRT  
ORGANISM: Conus nobilis  
US-10-072-602B-609

Query Match 30.1%; Score 37; DB 14; Length 17;  
Best Local Similarity 40.0%; Pred. No. 2.2e+02;  
Matches 6; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 5 CCLIPACRRNHKKFC 19  
||| :  
DB 2 CCERPPCRWQNPDLG 16

RESULT 30  
US-09-954-385-346  
Sequence 346, Application US/09954385  
Publication No. US20030100467A1  
GENERAL INFORMATION:  
APPLICANT: Aehle, Wolfgang  
APPLICANT: Baldwin, Toby L.  
APPLICANT: Van Gastel, Franciscus J.C.  
APPLICANT: Janssen, Giselle G.  
APPLICANT: Murray, Christopher J.  
APPLICANT: Wang, Huaming  
APPLICANT: Winetzkzy, Deborah S.  
TITLE OF INVENTION: Binding Phenol Oxidizing Enzyme-peptide  
FILE REFERENCE: GC690  
CURRENT APPLICATION NUMBER: US/09/954,385  
CURRENT FILING DATE: 2001-09-12  
NUMBER OF SEQ ID NOS: 433  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 346  
LENGTH: 12  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: binding peptide  
US-09-954-385-346

Query Match 29.3%; Score 36; DB 10; Length 12;  
Best Local Similarity 83.3%; Pred. No. 2.2e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 RCCLIP 9  
||| :  
DB 7 RCCLLP 12

RESULT 31  
US-09-910-009A-170  
Sequence 170, Application US/09910009A  
Publication No. US20030050234A1  
GENERAL INFORMATION:  
APPLICANT: University of Utah Research Foundation  
APPLICANT: Cognetix, Inc.  
APPLICANT: Olivera, Baldomero M.  
APPLICANT: McIntosh, J. Michael  
APPLICANT: Garrett, James E.  
APPLICANT: Watkins, Maren  
APPLICANT: Cruz, Lourdes J.  
APPLICANT: Shon, Ki-Joon  
APPLICANT: Jacobsen, Richard

APPLICANT: Jones, Robert M.  
APPLICANT: Cartier, G. Edward  
APPLICANT: Shen, Greg S.  
APPLICANT: Wagstaff, John D.  
TITLE OF INVENTION: Mu-Conopeptides  
FILE REFERENCE: 2314-242  
CURRENT FILING DATE: 2001-07-23  
PRIORITY APPLICATION NUMBER: US 60/219,619  
PRIORITY FILING DATE: 2000-07-21  
PRIORITY APPLICATION NUMBER: US 60/245,157  
PRIORITY FILING DATE: 2000-11-03  
PRIORITY APPLICATION NUMBER: US 60/264,319  
PRIORITY FILING DATE: 2001-01-29  
PRIORITY APPLICATION NUMBER: US 60/277,270  
PRIORITY FILING DATE: 2001-03-21  
NUMBER OF SEQ ID NOS: 520  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 170  
LENGTH: 16  
TYPE: PRT  
ORGANISM: Conus marmoreus  
FEATURE:  
NAME/KEY: PEPTIDE  
LOCATION: (1)..(16)  
OTHER INFORMATION: Xaa at residue 4 and 13 is Pro or Hyp  
-09-910-009A-170  
Query Match 29.3%; Score 36; DB 10; Length 16;  
Best Local Similarity 40.0%; Pred. No. 2.8e+02;  
Matches 6; Conservative 1; Mismatches 8; Indels 0; Gaps 0;  
5 CCLIPACRNHHKFC 19  
1 CCXASACRLGCRXCC 15  
SULT 32  
-09-910-009A-171  
Sequence 171, Application US/09910009A  
Publication No. US20030050234A1  
GENERAL INFORMATION:  
APPLICANT: University of Utah Research Foundation  
APPLICANT: Cognetix, Inc.  
APPLICANT: Olivera, Baldomero M.  
APPLICANT: McIntosh, J. Michael  
APPLICANT: Garrett, James E.  
APPLICANT: Watkins, Maren  
APPLICANT: Cruz, Lourdes J.  
APPLICANT: Shon, Ki-Joon  
APPLICANT: Jacobsen, Richard  
APPLICANT: Jones, Robert M.  
APPLICANT: Cartier, G. Edward  
APPLICANT: Shen, Greg S.  
APPLICANT: Wagstaff, John D.  
TITLE OF INVENTION: Mu-Conopeptides  
FILE REFERENCE: 2314-242  
CURRENT FILING DATE: 2001-07-23  
PRIORITY APPLICATION NUMBER: US 60/219,619  
PRIORITY FILING DATE: 2000-07-21  
PRIORITY APPLICATION NUMBER: US 60/245,157  
PRIORITY FILING DATE: 2000-11-03  
PRIORITY APPLICATION NUMBER: US 60/264,319  
PRIORITY FILING DATE: 2001-01-29  
PRIORITY APPLICATION NUMBER: US 60/277,270  
PRIORITY FILING DATE: 2001-03-21  
NUMBER OF SEQ ID NOS: 520  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 171  
LENGTH: 16  
TYPE: PRT  
ORGANISM: Conus marmoreus

FEATURE:  
NAME/KEY: PEPTIDE  
LOCATION: (1)..(16)  
OTHER INFORMATION: Xaa at residue 4 and 13 is Pro or Hyp  
US-09-910-009A-171  
Query Match 29.3%; Score 36; DB 10; Length 16;  
Best Local Similarity 40.0%; Pred. No. 2.8e+02;  
Matches 6; Conservative 1; Mismatches 8; Indels 0; Gaps 0;  
5 CCLIPACRNHHKFC 19  
1 CCXASACRLGCRXCC 15  
Db  
US-09-910-009A-172  
Sequence 172, Application US/09910009A  
Publication No. US20030050234A1  
GENERAL INFORMATION:  
APPLICANT: University of Utah Research Foundation  
APPLICANT: Cognetix, Inc.  
APPLICANT: Olivera, Baldomero M.  
APPLICANT: McIntosh, J. Michael  
APPLICANT: Garrett, James E.  
APPLICANT: Watkins, Maren  
APPLICANT: Cruz, Lourdes J.  
APPLICANT: Shon, Ki-Joon  
APPLICANT: Jacobsen, Richard  
APPLICANT: Jones, Robert M.  
APPLICANT: Cartier, G. Edward  
APPLICANT: Shen, Greg S.  
APPLICANT: Wagstaff, John D.  
TITLE OF INVENTION: Mu-Conopeptides  
FILE REFERENCE: 2314-242  
CURRENT FILING DATE: 2001-07-23  
PRIORITY APPLICATION NUMBER: US 60/219,619  
PRIORITY FILING DATE: 2000-07-21  
PRIORITY APPLICATION NUMBER: US 60/245,157  
PRIORITY FILING DATE: 2000-11-03  
PRIORITY APPLICATION NUMBER: US 60/264,319  
PRIORITY FILING DATE: 2001-01-29  
PRIORITY APPLICATION NUMBER: US 60/277,270  
PRIORITY FILING DATE: 2001-03-21  
NUMBER OF SEQ ID NOS: 520  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 172  
LENGTH: 16  
TYPE: PRT  
ORGANISM: Conus marmoreus  
FEATURE:  
NAME/KEY: PEPTIDE  
LOCATION: (1)..(16)  
OTHER INFORMATION: Xaa at residue 4 and 13 is Pro or Hyp  
US-09-910-009A-172  
Query Match 29.3%; Score 36; DB 10; Length 16;  
Best Local Similarity 40.0%; Pred. No. 2.8e+02;  
Matches 6; Conservative 1; Mismatches 8; Indels 0; Gaps 0;  
5 CCLIPACRNHHKFC 19  
1 CCXASACRLGCRXCC 15  
Db  
US-09-910-009A-442  
Sequence 442, Application US/09910009A  
Publication No. US20030050234A1  
GENERAL INFORMATION:  
APPLICANT: University of Utah Research Foundation  
APPLICANT: Cognetix, Inc.

APPLICANT: Olivera, Baldomero M.  
APPLICANT: McIntosh, J. Michael  
APPLICANT: Garrett, James E.  
APPLICANT: Watkins, Maren  
APPLICANT: Cruz, Lourdes J.  
APPLICANT: Shon, Ki-oon  
APPLICANT: Jacobsen, Richard  
APPLICANT: Jones, Robert M.  
APPLICANT: Cartier, G. Edward  
APPLICANT: Shen, Greg S.  
APPLICANT: Wagstaff, John D.  
TITLE OF INVENTION: Mu-Conopeptides  
FILE REFERENCE: 2314-242  
CURRENT APPLICATION NUMBER: US/09/910,009A  
CURRENT FILING DATE: 2001-07-23  
PRIOR APPLICATION NUMBER: US 60/219,619  
PRIOR FILING DATE: 2000-07-21  
PRIOR APPLICATION NUMBER: US 60/245,157  
PRIOR FILING DATE: 2000-11-03  
PRIOR APPLICATION NUMBER: US 60/264,319  
PRIOR FILING DATE: 2001-01-29  
PRIOR APPLICATION NUMBER: US 60/277,270  
PRIOR FILING DATE: 2001-03-21  
NUMBER OF SEQ ID NOS: 520  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 442  
LENGTH: 16  
TYPE: PRT  
ORGANISM: Conus marmoreus  
FEATURE:  
NAME/KEY: PEPTIDE  
LOCATION: (1)..(16)  
OTHER INFORMATION: Xaa is Hyp  
-09-910-009A-442

Query Match 29.3%; Score 36; DB 10; Length 16;  
Best Local Similarity 40.0%; Pred. No. 2.8e+02;  
Matches 6; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

5 CCLIPACGRNKKKFC 19  
|||  
1 CCAXSACRLGCRXC 15

SULT 35  
-10-072-602B-429  
Sequence 429, Application US/10072602B  
Publication No. US20030109670A1  
GENERAL INFORMATION:  
APPLICANT: University of Utah Research Foundation  
APPLICANT: Cognetix, Inc.  
APPLICANT: Olivera, Baldomero M.  
APPLICANT: McIntosh, J. Michael  
APPLICANT: Watkins, Maren  
APPLICANT: Garrett, James E.  
APPLICANT: Cruz, Lourdes J.  
APPLICANT: Grilley, Michelle  
APPLICANT: Schoenfeld, Robert M.  
APPLICANT: Walker, Craig  
APPLICANT: Shetty, Reshma  
APPLICANT: Jones, Robert M.  
TITLE OF INVENTION: Cone Snail Peptides  
FILE REFERENCE: 2314-249  
CURRENT APPLICATION NUMBER: US/10/072,602B  
CURRENT FILING DATE: 2002-02-11  
PRIOR APPLICATION NUMBER: US 60/267,408  
PRIOR FILING DATE: 2001-02-09  
NUMBER OF SEQ ID NOS: 638  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 429  
LENGTH: 16  
TYPE: PRT  
ORGANISM: Conus leopardus

FEATURE:  
NAME/KEY: PEPTIDE  
LOCATION: (1)..(16)  
OTHER INFORMATION: Xaa at residues 5 and 12 is Pro or hydroxy-Pro; Xaa at residue 1 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr  
US-10-072-602B-429

Query Match 29.3%; Score 36; DB 14; Length 16;  
Best Local Similarity 40.0%; Pred. No. 2.8e+02;  
Matches 6; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 5 CCLIPACGRNKKKFC 19  
DB 1 CCSNXACNRXNKAIC 15

Search completed: February 18, 2004, 06:34:10  
Job time : 35 secs

GenCore version 5.1.6  
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protein - protein search, using sw model

on: February 18, 2004, 06:26:29 ; Search time 23 Seconds  
(without alignments)  
42.648 Million cell updates/sec

le: US-09-806-376-1

fect score: 123

quence: 1 FNRCCLPACRHHKFC 19

ring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

arched: 389414 seqs, 51625971 residues

tal number of hits satisfying chosen parameters: 166134

nimum DB seq length: 0

ximum DB seq length: 19

st-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 50 summaries

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- 1: /cgn2\_6/prodata/2/aa/5A\_COMB.pep:\*
- 2: /cgn2\_6/prodata/2/aa/5B\_COMB.pep:\*
- 3: /cgn2\_6/prodata/2/aa/6A\_COMB.pep:\*
- 4: /cgn2\_6/prodata/2/aa/6B\_COMB.pep:\*
- 5: /cgn2\_6/prodata/2/aa/PCUTS\_COMB.pep:\*
- 6: /cgn2\_6/prodata/2/aa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

sult No.	Score	Query Match	Length	DB ID	Description
1	48	39.0	16	3	US-09-219-446B-9
2	47	38.2	16	3	US-09-219-446B-10
3	46	37.4	18	1	US-08-137-800-32
4	46	37.4	18	1	US-08-477-383-32
5	46	37.4	18	1	US-08-487-174-32
6	46	37.4	18	1	US-08-480-750-32
7	44	35.8	16	1	US-08-477-383-54
8	44	35.8	16	1	US-08-487-174-54
9	44	35.8	16	1	US-08-480-750-54
10	44	35.8	16	3	US-09-219-446B-2
11	44	35.8	17	3	US-09-219-446B-3
12	44	35.8	19	1	US-08-084-848A-8
13	44	35.8	19	1	US-08-458-499-8
14	43	35.0	16	3	US-09-219-446B-11
15	43	35.0	19	4	US-09-136-769A-3
16	43	35.0	19	4	US-09-136-769A-14
17	42	34.1	16	3	US-09-219-446B-4
18	42	34.1	16	3	US-09-219-446B-12
19	41	33.3	16	1	US-08-137-800-17
20	41	33.3	16	1	US-08-477-383-17
21	41	33.3	16	1	US-08-487-174-17
22	41	33.3	16	1	US-08-480-750-17
23	40	32.5	14	1	US-08-116-733-7
24	40	32.5	14	1	US-08-469-615-5
25	40	32.5	14	1	US-08-466-763-5
26	40	32.5	14	2	US-08-411-142A-5
27	40	32.5	16	1	US-08-137-800-15

Sequence 15, Appl  
Sequence 15, Appl  
Sequence 15, Appl  
Sequence 13, Appl  
Sequence 31, Appl  
Sequence 13, Appl  
Sequence 13, Appl  
Sequence 13, Appl  
Sequence 31, Appl  
Sequence 13, Appl  
Sequence 13, Appl  
Sequence 13, Appl  
Sequence 31, Appl  
Sequence 13, Appl  
Sequence 13, Appl  
Sequence 20, Appl  
Sequence 20, Appl  
Sequence 20, Appl  
Sequence 20, Appl  
Sequence 2, Appl  
Sequence 5, Appl  
Sequence 6, Appl  
Sequence 7, Appl  
Sequence 7, Appl  
Sequence 7, Appl  
Sequence 4, Appl

ALIGNMENTS

RESULT 1

US-09-219-446B-9  
; Sequence 9, Application US/09219446B  
; Patent No. 6265541  
; GENERAL INFORMATION:  
; APPLICANT: Oliveira, Baldomero M.  
; APPLICANT: McIntosh, J. Michael  
; APPLICANT: Yoshikami, Doju  
; APPLICANT: Cartier, G. Edward  
; APPLICANT: Luo, Sigun  
; APPLICANT: University of Utah Research Foundation  
; TITLE OF INVENTION: Uses of Alpha-Conotoxin Peptides  
; FILE REFERENCE: Uses of Alpha-Conotoxins  
; CURRENT APPLICATION NUMBER: US/09/219,446B  
; CURRENT FILING DATE: 1998-12-23  
; PRIOR APPLICATION NUMBER: US 60/080,588  
; PRIOR FILING DATE: 1998-04-03  
; PRIOR APPLICATION NUMBER: US 60/070,153  
; PRIOR FILING DATE: 1997-12-31  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 9  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Conus purpurascens  
US-09-219-446B-9

Query Match 39.0%; Score 48; DB 3; Length 16;  
Best Local Similarity 40.0%; Pred. No. 3.9;  
Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 5 CCLIPACRHHKFC 19

Db 2 CCSLPACRHHKFC 16

RESULT 2

US-09-219-446B-10  
; Sequence 10, Application US/09219446B  
; Patent No. 6265541  
; GENERAL INFORMATION:  
; APPLICANT: Oliveira, Baldomero M.  
; APPLICANT: McIntosh, J. Michael  
; APPLICANT: Yoshikami, Doju  
; APPLICANT: Cartier, G. Edward

APPLICANT: Luo, Siqin  
APPLICANT: University of Utah Research Foundation  
TITLE OF INVENTION: Uses of Alpha-Conotoxin Peptides  
FILE REFERENCE: Uses of Alpha-Conotoxins  
CURRENT APPLICATION NUMBER: US/09/219,446B  
CURRENT FILING DATE: 1998-12-23  
PRIOR APPLICATION NUMBER: US 60/080,588  
PRIOR FILING DATE: 1998-04-03  
PRIOR APPLICATION NUMBER: US 60/070,153  
PRIOR FILING DATE: 1997-12-31  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: Patent in Ver. 2.0  
SEQ ID NO 10  
LENGTH: 16  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: A10L derivative  
OTHER INFORMATION: of C. purpurascens Fh1A  
-09-219-446B-10

Query Match 38.2%; Score 47; DB 3; Length 16;  
Best Local Similarity 40.0%; Pred. No. 5-2;  
Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;  
5 CCLIPACRRNHKKFC 19  
|||:|:|:|:|:  
2 CCSLPPCALNPDYC 16

RESULT 3  
-08-137-800-32  
Sequence 32, Application US/08137800  
Patent No. 5514774  
GENERAL INFORMATION:  
APPLICANT: Olivera, Baldomero M.  
APPLICANT: Cruz, Lourdes J.  
APPLICANT: Hillyard, David R.  
APPLICANT: McIntosh, J. Michael  
APPLICANT: Santos, Ameurfin S.  
TITLE OF INVENTION: Conotoxin Peptides  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Venable, Baetjer, Howard & Civiletti  
STREET: 1201 New York Avenue N.W., Suite 1000  
CITY: Washington  
STATE: DC  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/137,800  
FILING DATE: 19-OCT-1993  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Ihnen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: 24260-104763  
TELEPHONE: 202-962-4810  
TELEFAX: 202-962-8300  
INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:

ORGANISM: Conus ermineus  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 3  
OTHER INFORMATION: /note= "Xaa is Pro or Hydroxy-Pro"  
US-08-137-800-32  
Query Match 37.4%; Score 46; DB 1; Length 18;  
Best Local Similarity 46.7%; Pred. No. 7-7;  
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;  
5 CCLIPACRRNHKKFC 19  
|||:|:|:|:|:  
4 CCSNPACVNNPQIC 18  
Db  
RESULT 4  
US-08-477-383-32  
Sequence 32, Application US/08477383  
Patent No. 5589340  
GENERAL INFORMATION:  
APPLICANT: Olivera, Baldomero M.  
APPLICANT: Cruz, Lourdes J.  
APPLICANT: Hillyard, David R.  
APPLICANT: Macintosh, J. Michael  
APPLICANT: Santos, Ameurfin S.  
TITLE OF INVENTION: Conotoxin Peptides  
NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Venable, Baetjer, Howard & Civiletti  
STREET: 1201 New York Avenue, N.W., Suite 1000  
CITY: Washington  
STATE: DC  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/477,383  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/137,800  
FILING DATE: 19-OCT-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/084,848  
FILING DATE: 29-JUN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Ihnen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: 24260-107673  
TELEPHONE: 202-962-4810  
TELEFAX: 202-962-8300  
INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
ORGANISM: Conus ermineus  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 3  
OTHER INFORMATION: /note= "Xaa is Pro or Hydroxy-Pro."  
FEATURE:  
NAME/KEY: Modified-site



LOCATION: 18  
OTHER INFORMATION: /note= "The C-terminus is  
OTHER INFORMATION: preferably amidated."  
08-477-383-32

Query Match 37.4%; Score 46; DB 1; Length 18;  
Best Local Similarity 46.7%; Pred. No. 7.7;  
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 5 CCLIPACRRNHKKFC 19  
||| : :  
DB 4 CCSNPACVNVNPQIC 18

RESULT 6  
US-08-480-750-32  
; Sequence 32, Application US/08480750  
; Patent No. 5633347  
; GENERAL INFORMATION:  
; APPLICANT: Olivera, Baldomero M.  
; APPLICANT: Cruz, Lourdes J.  
; APPLICANT: Hillyard, David R.  
; APPLICANT: Macintosh, J. Michael  
; APPLICANT: Santos, Ameurfino S.  
; TITLE OF INVENTION: Conotoxin Peptides  
; NUMBER OF SEQUENCES: 59  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti  
; STREET: 1201 New York Avenue, N.W., Suite 1000  
; CITY: Washington  
; STATE: DC  
; COUNTRY: U.S.A.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/480,750  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/137,800  
; FILING DATE: 19-OCT-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/084,848  
; FILING DATE: 29-JUN-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ihnen, Jeffrey L.  
; REGISTRATION NUMBER: 28,957  
; REFERENCE/DOCKET NUMBER: 24260-107673  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-962-4810  
; TELEFAX: 202-962-8300  
; INFORMATION FOR SEQ ID NO: 32:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Conus ermineus  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: 3  
; OTHER INFORMATION: /note= "Xaa is Pro or Hydroxy-Pro."  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: 18  
; OTHER INFORMATION: /note= "The C-terminus is  
; OTHER INFORMATION: preferably amidated."  
US-08-480-750-32

Query Match 37.4%; Score 46; DB 1; Length 18;  
Best Local Similarity 46.7%; Pred. No. 7.7;  
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

5 CCLIPACRRNHKFC 19  
||| | : :  
4 CCSNPACVNVNPQIC 18

## SULT 7

-08-477-383-54  
Sequence 54, Application US/08477383  
Patent No. 5589340  
GENERAL INFORMATION:  
APPLICANT: Olivera, Baldomero M.  
APPLICANT: Cruz, Lourdes J.  
APPLICANT: Hillyard, David R.  
APPLICANT: Macintosh, J. Michael  
APPLICANT: Santos, Ameurfino S.  
TITLE OF INVENTION: Conotoxin Peptides  
NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Venable, Baetjer, Howard & Civiletti  
STREET: 1201 New York Avenue, N.W., Suite 1000  
CITY: Washington  
STATE: DC  
COUNTRY: U.S.A.  
ZIP: 20005

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/477,383  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/137,800  
FILING DATE: 19-OCT-1993

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/084,848  
FILING DATE: 29-JUN-1993

ATTORNEY/AGENT INFORMATION:  
NAME: Ihnen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: 24260-107673  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-962-4810  
TELEFAX: 202-962-8300

INFORMATION FOR SEQ ID NO: 54:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid

STRANDEDNESS:  
TOPOLOGY: linear

MOLECULE TYPE: peptide  
HYPOTHETICAL: NO

ORIGINAL SOURCE:  
ORGANISM: Conus magus

FEATURE:  
NAME/KEY: Modified-site

LOCATION: 16

OTHER INFORMATION: /note= "The C-terminus is amidated."

-08-477-383-54

Query Match 35.8%; Score 44; DB 1; Length 16;  
Best Local Similarity 40.0%; Pred. No. 13;  
Matches 6; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

5 CCLIPACRRNHKFC 19

Db 2 CCSNPVCHLEHSNLC 16

## RESULT 8

US-08-487-174-54  
Sequence 54, Application US/08487174  
Patent No. 5595972  
GENERAL INFORMATION:  
APPLICANT: Olivera, Baldomero M.  
APPLICANT: Cruz, Lourdes J.  
APPLICANT: Hillyard, David R.  
APPLICANT: Macintosh, J. Michael  
APPLICANT: Santos, Ameurfino S.  
TITLE OF INVENTION: Conotoxin Peptides  
NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Venable, Baetjer, Howard & Civiletti  
STREET: 1201 New York Avenue, N.W., Suite 1000  
CITY: Washington  
STATE: DC  
COUNTRY: U.S.A.  
ZIP: 20005

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/487,174  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 514

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/137,800  
FILING DATE: 19-OCT-1993

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/084,848  
FILING DATE: 29-JUN-1993

ATTORNEY/AGENT INFORMATION:  
NAME: Ihnen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: 24260-107673  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-962-4810  
TELEFAX: 202-962-8300

INFORMATION FOR SEQ ID NO: 54:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid

STRANDEDNESS:  
TOPOLOGY: linear

MOLECULE TYPE: peptide  
HYPOTHETICAL: NO

ORIGINAL SOURCE:  
ORGANISM: Conus magus

FEATURE:  
NAME/KEY: Modified-site

LOCATION: 16

OTHER INFORMATION: /note= "The C-terminus is amidated."

US-08-487-174-54

Query Match 35.8%; Score 44; DB 1; Length 16;  
Best Local Similarity 40.0%; Pred. No. 13;  
Matches 6; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 5 CCLIPACRRNHKFC 19

Db 2 CCSNPVCHLEHSNLC 16

## RESULT 9

US-08-480-750-54

Sequence 54, Application US/08480750  
Patent No. 5633347

## GENERAL INFORMATION:

APPLICANT: Olivera, Baldomero M.  
APPLICANT: Cruz, Lourdes J.  
APPLICANT: Hilliard, David R.  
APPLICANT: McIntosh, J. Michael  
APPLICANT: Santos, Aneurfino S.  
TITLE OF INVENTION: Conotoxin Peptides

NUMBER OF SEQUENCES: 59

## CORRESPONDENCE ADDRESS:

ADDRESSEE: Venable, Baetjer, Howard & Civiletti  
STREET: 1201 New York Avenue, N.W., Suite 1000  
CITY: Washington  
STATE: DC  
COUNTRY: U.S.A.  
ZIP: 20005

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30

## CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/480,750  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 530

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/137,800  
FILING DATE: 19-OCT-1993  
APPLICATION NUMBER: US 08/084,848  
FILING DATE: 29-JUN-1993

## ATTORNEY/AGENT INFORMATION:

NAME: Ihnen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: 24260-107673  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-962-4810  
TELEFAX: 202-962-8300

## INFORMATION FOR SEQ ID NO: 54:

## SEQUENCE CHARACTERISTICS:

LENGTH: 16 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

ORIGINAL SOURCE:

ORGANISM: Conus magus

FEATURE:

NAME/KEY: Modified-site

LOCATION: 16

OTHER INFORMATION: /note= "The C-terminus is

amidated."

-08-480-750-54

Query Match 35.8%; Score 44; DB 1; Length 16;  
Best Local Similarity 40.0%; Pred. No. 13;  
Matches 6; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 5 CCLIPACRRNHKKFC 19  
DB 2 CCSNPVCHLEHSLC 16

RESULT 10  
US-09-219-446B-2  
Sequence 2, Application US/09219446B  
Patent No. 6265541

## GENERAL INFORMATION:

APPLICANT: Olivera, Baldomero M.  
APPLICANT: McIntosh, J. Michael  
APPLICANT: Yoshikami, Doju

APPLICANT: Cartier, G. Edward  
APPLICANT: Luo, Siqin  
APPLICANT: University of Utah Research Foundation  
TITLE OF INVENTION: Uses of Alpha-Conotoxin Peptides

FILE REFERENCE: Uses of Alpha-Conotoxins

CURRENT APPLICATION NUMBER: US/09/219,446B

CURRENT FILING DATE: 1998-12-23

PRIOR APPLICATION NUMBER: US 60/080,588

PRIOR FILING DATE: 1998-04-03

PRIOR APPLICATION NUMBER: US 60/070,153

PRIOR FILING DATE: 1997-12-31

NUMBER OF SEQ ID NOS: 13

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 2

LENGTH: 16

TYPE: PRT

ORGANISM: Conus magus

US-09-219-446B-2

Query Match 35.8%; Score 44; DB 3; Length 16;  
Best Local Similarity 40.0%; Pred. No. 13;  
Matches 6; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 5 CCLIPACRRNHKKFC 19  
DB 2 CCSNPVCHLEHSLC 16

RESULT 11  
US-09-219-446B-3  
Sequence 3, Application US/09219446B  
Patent No. 6265541

## GENERAL INFORMATION:

APPLICANT: Olivera, Baldomero M.

APPLICANT: McIntosh, J. Michael

APPLICANT: Yoshikami, Doju

APPLICANT: Cartier, G. Edward

APPLICANT: Luo, Siqin

APPLICANT: University of Utah Research Foundation

TITLE OF INVENTION: Uses of Alpha-Conotoxin Peptides

FILE REFERENCE: Uses of Alpha-Conotoxins

CURRENT APPLICATION NUMBER: US/09/219,446B

CURRENT FILING DATE: 1998-12-23

PRIOR APPLICATION NUMBER: US 60/080,588

PRIOR FILING DATE: 1998-04-03

PRIOR APPLICATION NUMBER: US 60/070,153

PRIOR FILING DATE: 1997-12-31

NUMBER OF SEQ ID NOS: 13

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 3

LENGTH: 17

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Tyr derivative

OTHER INFORMATION: of C. magus MII

US-09-219-446B-3

Query Match 35.8%; Score 44; DB 3; Length 17;  
Best Local Similarity 40.0%; Pred. No. 13;  
Matches 6; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 5 CCLIPACRRNHKKFC 19  
DB 3 CCSNPVCHLEHSLC 17

RESULT 12  
US-08-084-848A-8  
Sequence 8, Application US/08084848A  
Patent No. 5432155

## GENERAL INFORMATION:

APPLICANT: Olivera, Baldomero M.

APPLICANT: Rivier, Jean E. F.  
APPLICANT: Cruz, Lourdes J.  
APPLICANT: Abogadie, Fe  
APPLICANT: Hopkins, Chris E.  
APPLICANT: Dykert, John  
APPLICANT: Torres, Josep L.  
TITLE OF INVENTION: Conotoxins I  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fitch, Even, Tabin & Flannery  
STREET: 135 South LaSalle Street, Suite 900  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/084,848A  
FILING DATE: June 29, 1993  
CLASSIFICATION: 535  
ATTORNEY/AGENT INFORMATION:  
NAME: Schumann, James J.  
REGISTRATION NUMBER: 20856  
REFERENCE/DOCKET NUMBER: 52511  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619)552-1311  
TELEFAX: (619)552-0095  
TELEX: 20 6566 PATLAW CGO  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-084-848A-8

Query Match 35.8%; Score 44; DB 1; Length 19;  
Best Local Similarity 40.0%; Pred. No. 15;  
Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 5 CCLIPACRRNHKKFC 19  
DB 2 CCSHPACSGKYQXC 16

RESULT 13  
US-08-458-499-8  
Sequence 8, Application US/08458499  
Patent No. 5700778  
GENERAL INFORMATION:  
APPLICANT: Olivera, Baldomero M.  
APPLICANT: Rivier, Jean E. F.  
APPLICANT: Cruz, Lourdes J.  
APPLICANT: Abogadie, Fe  
APPLICANT: Hopkins, Chris E.  
APPLICANT: Dykert, John  
APPLICANT: Torres, Josep L.  
TITLE OF INVENTION: Conotoxins I  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fitch, Even, Tabin & Flannery  
STREET: 135 South LaSalle Street, Suite 900  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/458,499  
FILING DATE: 02-JUN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/084,848  
FILING DATE: June 29, 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Schumann, James J.  
REGISTRATION NUMBER: 20856  
REFERENCE/DOCKET NUMBER: 52511  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619)552-1311  
TELEFAX: (619)552-0095  
TELEX: 20 6566 PATLAW CGO  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-458-499-8

Query Match 35.8%; Score 44; DB 1; Length 19;  
Best Local Similarity 40.0%; Pred. No. 15;  
Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 5 CCLIPACRRNHKKFC 19  
DB 2 CCSHPACSGKYQXC 16

RESULT 14  
US-09-219-446B-11  
Sequence 11, Application US/09219446B  
Patent No. 6265541  
GENERAL INFORMATION:  
APPLICANT: Olivera, Baldomero M.  
APPLICANT: McIntosh, J. Michael  
APPLICANT: Yoshikami, Doju  
APPLICANT: Cartier, G. Edward  
APPLICANT: Luo, Siglin  
APPLICANT: University of Utah Research Foundation  
TITLE OF INVENTION: Uses of Alpha-Conotoxin Peptides  
FILE REFERENCE: Uses of Alpha-Conotoxins  
CURRENT APPLICATION NUMBER: US/09/219,446B  
CURRENT FILING DATE: 1998-12-23  
PRIOR APPLICATION NUMBER: US 60/080,588  
PRIOR FILING DATE: 1998-04-03  
PRIOR APPLICATION NUMBER: US 60/070,153  
PRIOR FILING DATE: 1997-12-31  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 11  
LENGTH: 16  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: N11S derivative  
of C. purpurascens Pn1A  
US-09-219-446B-11

Query Match 35.0%; Score 43; DB 3; Length 16;  
Best Local Similarity 33.3%; Pred. No. 17;  
Matches 5; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 5 CCLIPACRRNHKKFC 19  
DB 2 CCSLPFCAASNPDC 16

ULT 15  
 09-136-769A-3  
 Sequence 3, Application US/09136769A  
 Patent No. 6307014  
 GENERAL INFORMATION:  
 APPLICANT: Furie, Bruce  
 APPLICANT: Furie, Barbara  
 APPLICANT: Stenflo, Johan  
 APPLICANT: Rigby, Alan C.  
 APPLICANT: Roepstoft, Peter  
 TITLE OF INVENTION: CONOPEPTIDES  
 FILE REFERENCE: 50065/002001  
 CURRENT APPLICATION NUMBER: US/09/136,769A  
 CURRENT FILING DATE: 1998-08-19  
 NUMBER OF SEQ ID NOS: 26  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 3  
 LENGTH: 19  
 TYPE: PRT  
 ORGANISM: Conus textile  
 FEATURE:  
 NAME/KEY: VARIANT  
 LOCATION: (2)...(16)  
 OTHER INFORMATION: Pro at position 2 is 4Hyp and each Xaa is  
 OTHER INFORMATION: Independently selected from Glu and  
 OTHER INFORMATION: gamma-carboxyglutamic acid, provided that at least  
 OTHER INFORMATION: one Xaa is gamma-carboxyglutamic acid.  
 NAME/KEY: VARIANT  
 LOCATION: (1)...(19)  
 OTHER INFORMATION: Xaa = Any Amino Acid  
 NAME/KEY: VARIANT  
 LOCATION: (1)...(19)  
 OTHER INFORMATION: Xaa = Any Amino Acid  
 09-136-769A-3  
 Query Match 35.0%; Score 43; DB 4; Length 19;  
 Best Local Similarity 40.0%; Pred. No. 20;  
 Matches 6; Conservative 1; Mismatches 8; Indels 0; Gaps 0;  
 5 CCLIPACRRNHKKFC 19  
 4 CCSDPRCNSHPXLC 18

LOCATION: (1)...(19)  
 OTHER INFORMATION: Xaa = Any Amino Acid  
 US-09-136-769A-14  
 Query Match 35.0%; Score 43; DB 4; Length 19;  
 Best Local Similarity 40.0%; Pred. No. 20;  
 Matches 6; Conservative 1; Mismatches 8; Indels 0; Gaps 0;  
 QY 5 CCLIPACRRNHKKFC 19  
 Db 4 CCSDPRCNSHPXLC 18  
 RESULT 17  
 US-09-219-446B-4  
 Sequence 4, Application US/09219446B  
 Patent No. 6265541  
 GENERAL INFORMATION:  
 APPLICANT: Olivera, Baldomero M.  
 APPLICANT: McIntosh, J. Michael  
 APPLICANT: Yoshikami, Doju  
 APPLICANT: Cartier, G. Edward  
 APPLICANT: Luo, Siglin  
 APPLICANT: University of Utah Research Foundation  
 TITLE OF INVENTION: Uses of Alpha-Conotoxin Peptides  
 FILE REFERENCE: Uses of Alpha-Conotoxins  
 CURRENT APPLICATION NUMBER: US/09/219,446B  
 CURRENT FILING DATE: 1998-12-23  
 PRIOR APPLICATION NUMBER: US 60/080,588  
 PRIOR FILING DATE: 1998-04-03  
 PRIOR APPLICATION NUMBER: US 60/070,153  
 PRIOR FILING DATE: 1997-12-31  
 NUMBER OF SEQ ID NOS: 13  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 4  
 LENGTH: 16  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Description of Artificial Sequence: FAT derivative  
 OTHER INFORMATION: of C. magus MII  
 US-09-219-446B-4  
 Query Match 34.1%; Score 42; DB 3; Length 16;  
 Best Local Similarity 40.0%; Pred. No. 23;  
 Matches 6; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
 QY 5 CCLIPACRRNHKKFC 19  
 Db 2 CCNPFVCFATHSNLC 16  
 RESULT 18  
 US-09-219-446B-12  
 Sequence 12, Application US/09219446B  
 Patent No. 6265541  
 GENERAL INFORMATION:  
 APPLICANT: Olivera, Baldomero M.  
 APPLICANT: McIntosh, J. Michael  
 APPLICANT: Yoshikami, Doju  
 APPLICANT: Cartier, G. Edward  
 APPLICANT: Luo, Siglin  
 APPLICANT: University of Utah Research Foundation  
 TITLE OF INVENTION: Uses of Alpha-Conotoxin Peptides  
 FILE REFERENCE: Uses of Alpha-Conotoxins  
 CURRENT APPLICATION NUMBER: US/09/219,446B  
 CURRENT FILING DATE: 1998-12-23  
 PRIOR APPLICATION NUMBER: US 60/080,588  
 PRIOR FILING DATE: 1998-04-03  
 PRIOR APPLICATION NUMBER: US 60/070,153  
 PRIOR FILING DATE: 1997-12-31  
 NUMBER OF SEQ ID NOS: 13  
 SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 12  
LENGTH: 16

TYPE: PRT  
ORGANISM: Conus purpurascens  
-09-219-446B-12

Query Match 34.1%; Score 42; DB 3; Length 16;  
Best Local Similarity 33.3%; Pred. No. 23;  
Matches 5; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

5 CCLIPACRRNHKKFC 19  
||:|:|:|:  
2 CGLSPFCALSNPDYC 16

SULT 19

US-08-137-800-17  
Sequence 17, Application US/08137800  
Patent No. 5514774  
GENERAL INFORMATION:

APPLICANT: Olivera, Baldomero M.  
APPLICANT: Cruz, Lourdes J.  
APPLICANT: Hillyard, David R.  
APPLICANT: McIntosh, J. Michael

TITLE OF INVENTION: Conotoxin Peptides  
NUMBER OF SEQUENCES: 53

CORRESPONDENCE ADDRESS:

ADDRESSEE: Venable, Baetjer, Howard & Civiletti  
STREET: 1201 New York Avenue N.W., Suite 1000  
CITY: Washington  
STATE: DC

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WordPerfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/137,800

FILING DATE: 19-OCT-1993

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Ihnen, Jeffrey L.

REGISTRATION NUMBER: 28,957

REFERENCE/DOCKET NUMBER: 24260-104763

TELEPHONE: 202-962-4810

TELEFAX: 202-962-8300

INFORMATION FOR SEQ ID NO: 17:

SEQUENCE CHARACTERISTICS:

LENGTH: 16 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Conus characteristicus

FEATURE:

NAME/KEY: Modified-site

LOCATION: 15..16

OTHER INFORMATION: /note= "Xaa is Ser or Asn"

-08-137-800-17

Query Match 33.3%; Score 41; DB 1; Length 16;  
Best Local Similarity 50.0%; Pred. No. 30;  
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

5 CCLIPACRRNHK 16  
||:|:|:|:  
3 CCGSPSCWCKYK 14

RESULT 20

US-08-477-383-17  
Sequence 17, Application US/08477383  
Patent No. 5589340  
GENERAL INFORMATION:

APPLICANT: Olivera, Baldomero M.  
APPLICANT: Cruz, Lourdes J.

APPLICANT: Hillyard, David R.

APPLICANT: Macintosh, J. Michael

APPLICANT: Santos, Ameurfin S.

TITLE OF INVENTION: Conotoxin Peptides

NUMBER OF SEQUENCES: 59

CORRESPONDENCE ADDRESS:

ADDRESSEE: Venable, Baetjer, Howard & Civiletti

STREET: 1201 New York Avenue, N.W., Suite 1000

CITY: Washington

STATE: DC

COUNTRY: U.S.A.

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/477,383

FILING DATE: 07-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/137,800

FILING DATE: 19-OCT-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/084,848

FILING DATE: 29-JUN-1993

ATTORNEY/AGENT INFORMATION:

NAME: Ihnen, Jeffrey L.

REGISTRATION NUMBER: 28,957

REFERENCE/DOCKET NUMBER: 24260-107673

TELEPHONE: 202-962-4810

TELEFAX: 202-962-8300

INFORMATION FOR SEQ ID NO: 17:

SEQUENCE CHARACTERISTICS:

LENGTH: 16 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

ORIGINAL SOURCE:

ORGANISM: Conus characteristicus

FEATURE:

NAME/KEY: Modified-site

LOCATION: 16

OTHER INFORMATION: /note= "Xaa is Ser or Asn."

US-08-477-383-17

Query Match 33.3%; Score 41; DB 1; Length 16;  
Best Local Similarity 50.0%; Pred. No. 30;  
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 5 CCLIPACRRNHK 16

||:|:|:|:

Db 3 CCGSPSCWCKYK 14

RESULT 21

US-08-487-174-17  
Sequence 17, Application US/08487174  
Patent No. 5595972

GENERAL INFORMATION:

APPLICANT: Olivera, Baldomero M.

APPLICANT: Cruz, Lourdes J.  
 APPLICANT: Hillyard, David R.  
 APPLICANT: Macintosh, J. Michael  
 APPLICANT: Santos, Ameurfin S.  
 TITLE OF INVENTION: Conotoxin Peptides  
 NUMBER OF SEQUENCES: 59  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Venable, Baetjer, Howard & Civiletti  
 STREET: 1201 New York Avenue, N.W., Suite 1000  
 CITY: Washington  
 STATE: DC  
 COUNTRY: U.S.A.  
 ZIP: 20005  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/487,174  
 FILING DATE: 07-JUN-1995  
 CLASSIFICATION: 514  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/137,800  
 FILING DATE: 19-OCT-1993  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/084,848  
 FILING DATE: 29-JUN-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Ihnen, Jeffrey L.  
 REGISTRATION NUMBER: 28,957  
 REFERENCE/DOCKET NUMBER: 24260-107673  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-962-4810  
 TELEFAX: 202-962-8300  
 INFORMATION FOR SEQ ID NO: 17:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 16 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 HYPOTHETICAL: NO  
 ORIGINAL SOURCE:  
 ORGANISM: Conus characteristic  
 FEATURE:  
 NAME/KEY: Modified-site  
 LOCATION: 16  
 OTHER INFORMATION: /note= "Xaa is Ser or Asn."  
 -08-487-174-17

Query Match 33.3%; Score 41; DB 1; Length 16;  
 Best Local Similarity 50.0%; Pred. No. 30;  
 Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
 5 CCLIPACRRNHK 16  
 3 CCSIPSCWEKYK 14

RESULT 22  
 -08-480-750-17  
 Sequence 17, Application US/08480750  
 Patent No. 5633347  
 GENERAL INFORMATION:  
 APPLICANT: Olivera, Baldomero M.  
 APPLICANT: Cruz, Lourdes J.  
 APPLICANT: Hillyard, David R.  
 APPLICANT: Macintosh, J. Michael  
 APPLICANT: Santos, Ameurfin S.  
 TITLE OF INVENTION: Conotoxin Peptides  
 NUMBER OF SEQUENCES: 59  
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Venable, Baetjer, Howard & Civiletti  
 STREET: 1201 New York Avenue, N.W., Suite 1000  
 CITY: Washington  
 STATE: DC  
 COUNTRY: U.S.A.  
 ZIP: 20005  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/480,750  
 FILING DATE: 07-JUN-1995  
 CLASSIFICATION: 530  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/137,800  
 FILING DATE: 19-OCT-1993  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/084,848  
 FILING DATE: 29-JUN-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Ihnen, Jeffrey L.  
 REGISTRATION NUMBER: 28,957  
 REFERENCE/DOCKET NUMBER: 24260-107673  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-962-4810  
 TELEFAX: 202-962-8300  
 INFORMATION FOR SEQ ID NO: 17:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 16 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 HYPOTHETICAL: NO  
 ORIGINAL SOURCE:  
 ORGANISM: Conus characteristic  
 FEATURE:  
 NAME/KEY: Modified-site  
 LOCATION: 16  
 OTHER INFORMATION: /note= "Xaa is Ser or Asn."  
 US-08-480-750-17

Query Match 33.3%; Score 41; DB 1; Length 16;  
 Best Local Similarity 50.0%; Pred. No. 30;  
 Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
 5 CCLIPACRRNHK 16  
 3 CCSIPSCWEKYK 14

RESULT 23  
 US-08-116-733-7  
 Sequence 7, Application US/08116733  
 Patent No. 5516632  
 GENERAL INFORMATION:  
 APPLICANT: PALKER, Thomas J.  
 APPLICANT: HAYNES, Barton F.  
 TITLE OF INVENTION: SYNTHETIC PEPTIDES  
 NUMBER OF SEQUENCES: 46  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: NIXON & VANDERHUYE P.C.  
 STREET: 1100 NORTH GLEBE ROAD  
 CITY: ARLINGTON  
 STATE: VIRGINIA  
 COUNTRY: U.S.A.  
 ZIP: 22201-4714  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/116,733  
FILING DATE: 07-SEP-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: WILSON, MARY J.  
REGISTRATION NUMBER: 32,955  
REFERENCE/DOCKET NUMBER: 1579-33  
TELEPHONE: (703) 816-4000  
TELEFAX: (703) 816-4100  
TELEX: 200797 NIXN UR  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
-08-116-733-7

Query Match 32.5%; Score 40; DB 1; Length 14;  
Best Local Similarity 54.5%; Pred. No. 37;  
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

1 FNRRCCLIPAC 11  
|||||  
4 FNTWTCDFQC 14

## SULT 24

-08-469-615-5  
Sequence 5, Application US/08469615  
Patent No. 5622703

GENERAL INFORMATION:  
APPLICANT: Berzofsky, Jay A.  
APPLICANT: Kurata, Akihiko  
TITLE OF INVENTION: Immunodominant Sites of HTLV-I Envelope  
TITLE OF INVENTION: Protein  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP  
STREET: P.O. Box 747  
CITY: Falls Church  
STATE: Virginia  
COUNTRY: USA  
ZIP: 22040-0747

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/469,615  
FILING DATE: 06-JUN-1995

CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/243,118  
FILING DATE: 16-MAY-1994

ATTORNEY/AGENT INFORMATION:  
NAME: Svensson, Leonard R.  
REGISTRATION NUMBER: 30330  
REFERENCE/DOCKET NUMBER: 1173-500P  
TELEPHONE: 703-205-8000  
TELEFAX: 703-205-8050

INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: not relevant  
MOLECULE TYPE: peptide

HYPOTHETICAL: NO  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE: HTLV-I  
ORGANISM: HTLV-I  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..14  
OTHER INFORMATION: /label= peptide\_sps  
US-08-469-615-5

Query Match 32.5%; Score 40; DB 1; Length 14;  
Best Local Similarity 54.5%; Pred. No. 37;  
Matches 6; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 FNRRCCLIPAC 11  
|||||  
Db 4 FNTWTCDFQC 14

## RESULT 25

US-08-466-763-5  
Sequence 5, Application US/08466763  
Patent No. 5695762  
GENERAL INFORMATION:  
APPLICANT: Berzofsky, Jay A.  
APPLICANT: Kurata, Akihiko  
TITLE OF INVENTION: Immunodominant Sites of HTLV-I Envelope  
TITLE OF INVENTION: Protein  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP  
STREET: P.O. Box 747  
CITY: Falls Church  
STATE: Virginia  
COUNTRY: USA  
ZIP: 22040-0747

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/466,763  
FILING DATE: 06-JUN-1995

CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/243,118  
FILING DATE: 16-MAY-1994

ATTORNEY/AGENT INFORMATION:  
NAME: Svensson, Leonard R.  
REGISTRATION NUMBER: 30330  
REFERENCE/DOCKET NUMBER: 1173-497P  
TELEPHONE: 703-205-8000  
TELEFAX: 703-205-8050

INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: not relevant  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE: HTLV-I  
ORGANISM: HTLV-I  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..14  
OTHER INFORMATION: /label= peptide\_sps  
US-08-466-763-5

Query Match 32.5%; Score 40; DB 1; Length 14;



Best Local Similarity 54.5%; Pred. No. 37;  
Matches 6; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

1 FNRRCCLIPAC 11  
||| |  
4 FNRWCFDPQC 14

SULT 26

-08-411-142A-5  
Sequence 5, Application US/08411142A  
Patent No. 5882853

GENERAL INFORMATION:

APPLICANT: Berzofsky, Jay A.  
APPLICANT: Kurata, Akiko  
TITLE OF INVENTION: METHOD OF EVALUATING HTLV-I-SPECIFIC  
TITLE OF INVENTION: T CELL RESPONSES  
NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 4225 Executive Square, Suite 1400  
CITY: La Jolla

STATE: CA

COUNTRY: US

ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows95

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/411,142A

FILING DATE: 27-MAR-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/243,118

FILING DATE: 16-MAY-1994

APPLICATION NUMBER: 07/401,411

FILING DATE: 01-SEP-1989

ATTORNEY/AGENT INFORMATION:

NAME: Wetherell, Jr., Ph.D, John R.

REGISTRATION NUMBER: 31,678

REFERENCE/DOCKET NUMBER: 08830/026002

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619/678-5070

TELEFAX: 619/678-5099

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 14 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: internal

IMMEDIATE SOURCE:

CLONE: HTLV-I

-08-411-142A-5

Query Match 32.5%; Score 40; DB 2; Length 14;  
Best Local Similarity 54.5%; Pred. No. 37;  
Matches 6; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

1 FNRRCCLIPAC 11  
||| |  
4 FNRWCFDPQC 14

SULT 27

-08-137-800-15

Sequence 15, Application US/08137800

Patent No. 5514774

GENERAL INFORMATION:

APPLICANT: Olivera, Baldomero M.

APPLICANT: Cruz, Lourdes J.  
APPLICANT: Hillyard, David R.  
APPLICANT: McIntosh, J. Michael  
APPLICANT: Santos, Ameurfin D.  
TITLE OF INVENTION: Conotoxin Peptides  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Venable, Baetjer, Howard & Civiletti  
STREET: 1201 New York Avenue N.W., Suite 1000  
CITY: Washington  
STATE: DC  
ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WordPerfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/137,800

FILING DATE: 19-OCT-1993

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Ihnen, Jeffrey L.

REGISTRATION NUMBER: 28,957

REFERENCE/DOCKET NUMBER: 24260-104763

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-962-4810

TELEFAX: 202-962-8300

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

LENGTH: 16 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Conus bandanus

FEATURE:

NAME/KEY: Modified-site

LOCATION: 6..13

OTHER INFORMATION: /note="Xaa(6) is Pro or

OTHER INFORMATION: Hydroxy-Pro; Xaa(13) is Pro or Hydroxy-Pro"

US-08-137-800-15

Query Match 32.5%; Score 40; DB 1; Length 16;  
Best Local Similarity 40.0%; Pred. No. 41;  
Matches 6; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 5 CCLIPACRRNHKFC 19  
||| |  
Db 2 COTHXACHVSHXELC 16

RESULT 28

US-08-477-383-15

Sequence 15, Application US/08477383

Patent No. 5589340

GENERAL INFORMATION:

APPLICANT: Olivera, Baldomero M.

APPLICANT: Cruz, Lourdes J.

APPLICANT: Hillyard, David R.

APPLICANT: Macintosh, J. Michael

APPLICANT: Santos, Ameurfin S.

TITLE OF INVENTION: Conotoxin Peptides

NUMBER OF SEQUENCES: 59

CORRESPONDENCE ADDRESS:

ADDRESSEE: Venable, Baetjer, Howard & Civiletti

STREET: 1201 New York Avenue, N.W., Suite 1000

CITY: Washington

STATE: DC

COUNTRY: U.S.A.

ZIP: 20005

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/477,383  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/137,800  
FILING DATE: 19-OCT-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/084,848  
FILING DATE: 29-JUN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Ihnen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: 24260-107673  
TELEPHONE: 202-962-4810  
TELEFAX: 202-962-8300  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
ORGANISM: Conus bandanus  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 16  
OTHER INFORMATION: /note= "The C-terminus is  
OTHER INFORMATION: preferably amidated."  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 6..13  
OTHER INFORMATION: /note= "Xaa(6) is Pro or  
OTHER INFORMATION: Hydroxy-Pro; Xaa(13) is Pro or Hydroxy-Pro."  
US-08-477-383-15  
Query Match 32.58; Score 40; DB 1; Length 16;  
Best Local Similarity 40.0%; Pred. No. 41;  
Matches 6; Conservative 2; Mismatches 7; Indels 0; Gaps 0;  
QY 5 CCLIPACRRNHKKFC 19  
DB 2 CCTXACHVSHXELC 16  
RESULT 29  
US-08-487-174-15  
Sequence 15, Application US/08487174  
Patent No. 5595972  
GENERAL INFORMATION:  
APPLICANT: Olivera, Baldomero M.  
APPLICANT: Cruz, Lourdes J.  
APPLICANT: Hillyard, David R.  
APPLICANT: Macintosh, J. Michael  
APPLICANT: Santos, Ameurfino S.  
TITLE OF INVENTION: Conotoxin Peptides  
NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Venable, Baetjer, Howard & Civiletti  
STREET: 1201 New York Avenue, N.W., Suite 1000  
CITY: Washington  
STATE: DC  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/487,174  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/137,800  
FILING DATE: 19-OCT-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/084,848  
FILING DATE: 29-JUN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Ihnen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: 24260-107673  
TELEPHONE: 202-962-4810  
TELEFAX: 202-962-8300  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
ORGANISM: Conus bandanus  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 16  
OTHER INFORMATION: /note= "The C-terminus is  
OTHER INFORMATION: preferably amidated."  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 6..13  
OTHER INFORMATION: /note= "Xaa(6) is Pro or  
OTHER INFORMATION: Hydroxy-Pro; Xaa(13) is Pro or Hydroxy-Pro."  
US-08-487-174-15  
Query Match 32.5%; Score 40; DB 1; Length 16;  
Best Local Similarity 40.0%; Pred. No. 41;  
Matches 6; Conservative 2; Mismatches 7; Indels 0; Gaps 0;  
QY 5 CCLIPACRRNHKKFC 19  
DB 2 CCTXACHVSHXELC 16  
RESULT 30  
US-08-480-750-15  
Sequence 15, Application US/08480750  
Patent No. 5633347  
GENERAL INFORMATION:  
APPLICANT: Olivera, Baldomero M.  
APPLICANT: Cruz, Lourdes J.  
APPLICANT: Hillyard, David R.  
APPLICANT: Macintosh, J. Michael  
APPLICANT: Santos, Ameurfino S.  
TITLE OF INVENTION: Conotoxin Peptides  
NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Venable, Baetjer, Howard & Civiletti  
STREET: 1201 New York Avenue, N.W., Suite 1000  
CITY: Washington  
STATE: DC  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/480,750  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/137,800  
FILING DATE: 19-OCT-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/084,848  
FILING DATE: 29-JUN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Ihnen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: 24260-107673  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-962-4810  
TELEFAX: 202-962-8300  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
ORGANISM: Conus bandanus  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 16  
OTHER INFORMATION: /note= "The C-terminus is  
OTHER INFORMATION: preferably amidated."  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 6-13  
OTHER INFORMATION: /note= "Xaa(6) is Pro or  
OTHER INFORMATION: Hydroxy-Pro; Xaa(13) is Pro or Hydroxy-Pro."  
-08-480-750-15  
Query Match 32.5%; Score 40; DB 1; Length 16;  
Best Local Similarity 40.0%; Pred. No. 41;  
Matches 6; Conservative 2; Mismatches 7; Indels 0; Gaps 0;  
5 CCLIPACRRNHKKFC 19  
|||:::  
2 CCTHXACHVSHXELC 16

SULT 31  
-08-137-800-13  
Sequence 13, Application US/08137800  
Patent No. 5514774  
GENERAL INFORMATION:  
APPLICANT: Olivera, Baldomero M.  
APPLICANT: Cruz, Lourdes J.  
APPLICANT: Hillyard, David R.  
APPLICANT: McIntosh, J. Michael  
APPLICANT: Santos, Ameurfin D.  
TITLE OF INVENTION: Conotoxin Peptides  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Venable, Baetjer, Howard & Civiletti  
STREET: 1201 New York Avenue N.W., Suite 1000  
CITY: Washington  
STATE: DC  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/137,800  
FILING DATE: 19-OCT-1993  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Ihnen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: 24260-104763  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-962-4810  
TELEFAX: 202-962-8300  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Conus ermineus  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 3-4  
OTHER INFORMATION: /note= "Xaa is Pro or Hydroxy-Pro"  
US-08-137-800-13  
Query Match 32.5%; Score 40; DB 1; Length 18;  
Best Local Similarity 33.3%; Pred. No. 45;  
Matches 5; Conservative 3; Mismatches 7; Indels 0; Gaps 0;  
QY 5 CCLIPACRRNHKKFC 19  
DB 4 CCYHETCNMNPQIC 18  
RESULT 32  
US-08-137-800-31  
Sequence 31, Application US/08137800  
Patent No. 5514774  
GENERAL INFORMATION:  
APPLICANT: Olivera, Baldomero M.  
APPLICANT: Cruz, Lourdes J.  
APPLICANT: Hillyard, David R.  
APPLICANT: McIntosh, J. Michael  
APPLICANT: Santos, Ameurfin D.  
TITLE OF INVENTION: Conotoxin Peptides  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Venable, Baetjer, Howard & Civiletti  
STREET: 1201 New York Avenue N.W., Suite 1000  
CITY: Washington  
STATE: DC  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/137,800  
FILING DATE: 19-OCT-1993  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Ihnen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: 24260-104763  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-962-4810  
TELEFAX: 202-962-8300  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:

LENGTH: 18 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Conus ermineus  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 3..4  
OTHER INFORMATION: /note= "Xaa is Pro or Hydroxy-Pro"  
3-08-137-800-31  
Query Match 32.5%; Score 40; DB 1; Length 18;  
Best Local Similarity 33.3%; Pred. No. 45;  
Matches 5; Conservative 3; Mismatches 7; Indels 0; Gaps 0;  
/ 5 CCLIPACRRNHKKFC 19  
4 CCYHPTCNMSNPQIC 18  
RESULT 33  
3-08-477-383-13  
Sequence 31, Application US/08477383  
Patent No. 5589340  
GENERAL INFORMATION:  
APPLICANT: Olivera, Baldomero M.  
APPLICANT: Cruz, Lourdes J.  
APPLICANT: Hillyard, David R.  
APPLICANT: Macintosh, J. Michael  
APPLICANT: Santos, Ameurfino S.  
TITLE OF INVENTION: Conotoxin Peptides  
NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Venable, Baetjer, Howard & Civiletti  
STREET: 1201 New York Avenue, N.W., Suite 1000  
CITY: Washington  
STATE: DC  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/477,383  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/137,800  
FILING DATE: 19-OCT-1993  
APPLICATION DATA:  
FILING DATE: 29-JUN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Ihnen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: 24260-107673  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-962-4810  
TELEFAX: 202-962-8300  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:

ORGANISM: Conus ermineus  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 3  
OTHER INFORMATION: /note= "Xaa is Pro or Hydroxy-Pro."  
US-08-477-383-13  
Query Match 32.5%; Score 40; DB 1; Length 18;  
Best Local Similarity 33.3%; Pred. No. 45;  
Matches 5; Conservative 3; Mismatches 7; Indels 0; Gaps 0;  
QV 5 CCLIPACRRNHKKFC 19  
DB 4 CCYHPTCNMSNPQIC 18  
RESULT 34  
US-08-477-383-31  
Sequence 31, Application US/08477383  
Patent No. 5589340  
GENERAL INFORMATION:  
APPLICANT: Olivera, Baldomero M.  
APPLICANT: Cruz, Lourdes J.  
APPLICANT: Hillyard, David R.  
APPLICANT: Macintosh, J. Michael  
APPLICANT: Santos, Ameurfino S.  
TITLE OF INVENTION: Conotoxin Peptides  
NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Venable, Baetjer, Howard & Civiletti  
STREET: 1201 New York Avenue, N.W., Suite 1000  
CITY: Washington  
STATE: DC  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/477,383  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/137,800  
FILING DATE: 19-OCT-1993  
APPLICATION DATA:  
FILING DATE: 29-JUN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Ihnen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: 24260-107673  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-962-4810  
TELEFAX: 202-962-8300  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
ORGANISM: Conus ermineus  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 3  
OTHER INFORMATION: /note= "Xaa is Pro or Hydroxy-Pro."  
FEATURE:  
NAME/KEY: Modified-site

LOCATION: 18  
OTHER INFORMATION: /note= "The C-terminus is  
OTHER INFORMATION: preferably amidated."  
;-08-477-383-31

Query Match 32.5%; Score 40; DB 1; Length 18;  
Best Local Similarity 33.3%; Pred. NO. 45;  
Matches 5; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

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4 CCYHPTCNMSNPQIC 18

## RESULT 35

;-08-487-174-13  
Sequence 13, Application US/08487174  
Patent No. 5595972

## GENERAL INFORMATION:

APPLICANT: Olivera, Baldomero M.  
APPLICANT: Cruz, Lourdes J.  
APPLICANT: Hillyard, David R.  
APPLICANT: Macintosh, J. Michael  
APPLICANT: Santos, Ameurfino S.  
TITLE OF INVENTION: Conotoxin Peptides  
NUMBER OF SEQUENCES: 59

## CORRESPONDENCE ADDRESS:

ADDRESSEE: Venable, Baetjer, Howard & Civiletti  
STREET: 1201 New York Avenue, N.W., Suite 1000  
CITY: Washington  
STATE: DC  
COUNTRY: U.S.A.  
ZIP: 20005

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/487,174  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 514

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/137,800  
FILING DATE: 19-OCT-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/084,848  
FILING DATE: 29-JUN-1993

## ATTORNEY/AGENT INFORMATION:

NAME: Ihnen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: 24260-107673  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-962-4810  
TELEFAX: 202-962-8300

## INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
STRANDEDNESS:

## TOPOLOGY: linear

## MOLECULE TYPE: peptide

## HYPOTHETICAL: NO

## ORIGINAL SOURCE:

## ORGANISM: Conus ermineus

## FEATURE:

## NAME/KEY: Modified-site

## LOCATION: 3

OTHER INFORMATION: /note= "Xaa is Pro or Hydroxy-Pro."  
;-08-487-174-13

## Query Match

Best Local Similarity 33.3%; Score 40; DB 1; Length 18;  
Matches 5; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Matches 5; Conservative 3; Mismatches 7; Indels 0; Gaps 0;  
Qy 5 CCLIPACRRNHKKFC 19  
Db 4 CCYHPTCNMSNPQIC 18

Search completed: February 18, 2004, 06:29:56  
Job time : 23 secs